

AMENDMENT

In the Specification:

Please insert a new paragraph on page 1, beginning at line 4, immediately before the heading "BACKGROUND OF THE INVENTION", as follows:

--SUBMISSION ON COMPACT DISC

The content of the following submission on compact discs is incorporated herein by reference in its entirety: A compact disc copy of the Sequence Listing (CRF) (file name: 514572002000, date recorded: June 9, 2006, size: 184,320 bytes); a duplicate compact disc copy of the Sequence Listing (COPY 1) (file name: 514572002000, date recorded: June 9, 2006, size: 184,320 bytes); and a duplicate compact disc copy of the Sequence Listing (COPY 2) (file name: 514572002000, date recorded: June 9, 2006, size: 184,320 bytes). --

Please replace Table 1, beginning on page 6, with a new Table 1 as follows:

Table 1. Exemplary Influenza A Virus Primers

| Id | Sequence | <u>SEQ ID NO:</u> |
|------------|--------------------------|-------------------|
| PMIA_00001 | TTTGTGCGACAATGCTTCA | <u>1</u> |
| PMIA_00002 | GACATTTGAGAAAGCTTGCC | <u>2</u> |
| PMIA_00003 | AGGGACAACCTNGAACCTGG | <u>3</u> |
| PMIA_00004 | AGGAGTTGAACCAAGACGCATT | <u>4</u> |
| PMIA_00005 | ACCACATTCCCTTATACTGGAG | <u>5</u> |
| PMIA_00006 | TTAGTCATCATCTTTCTCACAACA | <u>6</u> |
| PMIA_00007 | ACAAATTGCTTCAAATGAGAAC | <u>7</u> |
| PMIA_00008 | TGTCTCCGAAGAAATAAGATCC | <u>8</u> |
| PMIA_00009 | GCGCAGAGACTTGAAGATGT | <u>9</u> |
| PMIA_00010 | CCTTCCGTAGAAGGCCCT | <u>10</u> |

Please replace Table 2, beginning on page 6 and bridging to page 7, with a new Table 2 as follows:

Table 2. Exemplary Influenza B Virus Primers

| Id | Sequence | SEQ ID NO: |
|------------|--------------------------|------------|
| PMIB_00001 | CACAATGGCAGAATTTAGTGA | <u>11</u> |
| PMIB_00002 | GTCAGTTTGATCCCGTAGTG | <u>12</u> |
| PMIB_00003 | CAGATCCCAGAGTGGACTCA | <u>13</u> |
| PMIB_00004 | TGTATTACCCAAGGGTTGTTAC | <u>14</u> |
| PMIB_00005 | GATCAGCATGACAGTAACAGGA | <u>15</u> |
| PMIB_00006 | ATGTTCTGGTAAAAGTCGTTTAT | <u>16</u> |
| PMIB_00007 | CCACAGGGGAGATTCCAAAG | <u>17</u> |
| PMIB_00008 | GACATTCTTCCTGATTCATAATC | <u>18</u> |
| PMIB_00009 | CAAACAACGGTAGACCAATATA | <u>19</u> |
| PMIB_00010 | AGGTTCAGTATCTATCACAGTCTT | <u>20</u> |
| PMIB_00011 | ATGTCCAACATGGATATTGAC | <u>21</u> |
| PMIB_00012 | GCTCTTCCTATAAATCGAATG | <u>22</u> |
| PMIB_00013 | TGATCAAGTGATCGGAAGTAG | <u>23</u> |
| PMIB_00014 | GATGGTCTGCTTAATTGGAA | <u>24</u> |
| PMIB_00015 | ACAGAAGATGGAGAAGGCAA | <u>25</u> |
| PMIB_00016 | ATTGTTTCTTTGGCCTGGAT | <u>26</u> |

Please replace Table 3, beginning on page 7, with a new Table 3 as follows:

Table 3. Exemplary Human Metapneumovirus Primers

| Id | Sequence | SEQ ID NO: |
|-----------|-----------------------|------------|
| PMM_00001 | CATCCCCAAAAATTGCCAGAT | <u>27</u> |
| PMM_00002 | TTTGGGCTTTGCCTTAAATG | <u>28</u> |
| PMM_00003 | ACACCCTCATCATTGCAACA | <u>29</u> |
| PMM_00004 | GCCCTTCTGACTGTGGTCTC | <u>30</u> |

| <u>Id</u> | <u>Sequence</u> | <u>SEQ ID NO:</u> |
|------------|----------------------|-------------------|
| PMM_00005 | CGACACAGCAGCAGGAATTA | <u>31</u> |
| PMM_00006 | TCAAAGCTGCTTGACACTGG | <u>32</u> |
| PMM_00007 | CAAGTGCGACATTGATGACC | <u>33</u> |
| PMM_00008 | TAATTCCTGCTGCTGTGTCG | <u>34</u> |
| PMM_00009 | GCGACTGTAGCACTTGACGA | <u>35</u> |
| PMM_000010 | TCATGATCAGTCCCGCATAA | <u>36</u> |
| PMM_000011 | TGTTTCAGGCCAATACACCA | <u>37</u> |
| PMM_000012 | TCATGATCAGTCCCGCATAA | <u>38</u> |
| PMM_000013 | TCATGGGTAATGAAGCAGCA | <u>39</u> |
| PMM_000014 | GGAGTTTTCCTCATCTGGA | <u>40</u> |
| PMM_000015 | TCCAGTGATGGGAAAACCTC | <u>41</u> |
| PMM_000016 | TGTTGAGCTCCTTTGCCTTT | <u>42</u> |

Please replace Table 4, beginning on page 7 and bridging to page 9, with a new Table 4 as follows:

Table 4. Exemplary Human Adenovirus Primers

| <u>Id</u> | <u>Sequence</u> | <u>SEQ ID NO:</u> |
|--------------------------|----------------------|-------------------|
| PMA _d 1_00001 | TGGCGGTATAGGGTAACTG | <u>43</u> |
| PMA _d 1_00002 | ATTGCGGTGATGGTTAAAGG | <u>44</u> |
| PMA _d 1_00003 | TTTTGCCGATCCCACTTATC | <u>45</u> |
| PMA _d 1_00004 | GCAAGTCTACCACGGCATT | <u>46</u> |
| PMA _d 2_00001 | CTCCGTTATCGCTCCATGTT | <u>47</u> |
| PMA _d 2_00002 | AAGGACTGGTCGTTGGTGTC | <u>48</u> |
| PMA _d 2_00003 | AAATGCCGTGGTAGATTGTC | <u>49</u> |
| PMA _d 2_00004 | GTTGAAGGGGTTGACGTTGT | <u>50</u> |
| PMA _d 3_00001 | TCCTCTGGATGGCATAGGAC | <u>51</u> |

| <u>Id</u> | <u>Sequence</u> | <u>SEQ ID NO:</u> |
|--------------|----------------------|-------------------|
| PMAd3_00002 | TGTTGGTGTTAGTGGGCAA | <u>52</u> |
| PMAd3_00003 | ACATGGTCCTGCAAAGTTCC | <u>53</u> |
| PMAd3_00004 | GCATTGTGCCACGTTGTATC | <u>54</u> |
| PMAd4_00001 | CGCTTCGGAGTACCTCAGTC | <u>55</u> |
| PMAd4_00002 | CTGCATCATTGGTGTCAACC | <u>56</u> |
| PMAd4_00003 | GGCACCTTTTACCTCAACCA | <u>57</u> |
| PMAd4_00004 | TCTGGACCAAGAACCAGTCC | <u>58</u> |
| PMAd5_00001 | GGCCTACCCTGCTAACTTCC | <u>59</u> |
| PMAd5_00002 | ATAAAGAAGGGTGGGCTCGT | <u>60</u> |
| PMAd5_00003 | ATCGCAGTTGAATGCTGTTG | <u>61</u> |
| PMAd5_00004 | GTTGAAGGGGTTGACGTTGT | <u>62</u> |
| PMAd7_00001 | ACATGGTCCTGCAAAGTTCC | <u>63</u> |
| PMAd7_00002 | GATCGAACCCTGATCCAAGA | <u>64</u> |
| PMAd7_00003 | AACACCAACCGAAGGAGATG | <u>65</u> |
| PMAd7_00004 | CCTATGCCATCCAGAGGAAA | <u>66</u> |
| PMAd11_00001 | CAGATGCTCGCCAACTACAA | <u>67</u> |
| PMAd11_00002 | AGCCATGTAACCCACAAAGC | <u>68</u> |
| PMAd11_00003 | ACGGACGTTATGTGCCTTTC | <u>69</u> |
| PMAd11_00004 | GGGAATATTGGTTGCATTGG | <u>70</u> |
| PMAd21_00001 | ACTGGTTCCTGGTCCAGATG | <u>71</u> |
| PMAd21_00002 | AGCCATGTAACCCACAAAGC | <u>72</u> |
| PMAd21_00003 | CTGGATATGGCCAGCACTTT | <u>73</u> |
| PMAd21_00004 | CACCTGAGGTTCTGGTTGGT | <u>74</u> |

| <u>Id</u> | <u>Sequence</u> | <u>SEQ ID NO:</u> |
|--------------|----------------------|-------------------|
| PMAd23_00001 | TAATGAAAAGGGCGGACAAG | <u>75</u> |
| PMAd23_00002 | GCCAATGTAGTTTGGCCTGT | <u>76</u> |
| PMAd23_00003 | AACTCCGCGGTAGACAGCTA | <u>77</u> |
| PMAd23_00004 | CGTAGGTGTTGGTGTGGTG | <u>78</u> |

Please replace Table 5, beginning on page 9, with a new Table 5 as follows:

Table 5. Exemplary HCoV-OC229E Primers

| <u>Id</u> | <u>Sequence</u> | <u>SEQ ID NO:</u> |
|-----------|---|-------------------|
| PMV_a0053 | TCACTTGCTTCCGTTGAGGTTGGGCTGGCGGTTTAGAGTTGA | <u>79</u> |
| PMV_a0054 | GGTTTCGGATGTTACAGCGTGTCGACCGCCCTTGTTTATGG | <u>80</u> |
| PMV_a0055 | TCACTTGCTTCCGTTGAGGGCGTTGTTGGCCTTTTTCTTGTCT | <u>81</u> |
| PMV_a0056 | GGTTTCGGATGTTACAGCGTGCCCGGCATTATTTTCATTGTTCTG | <u>82</u> |
| PMV_a0057 | TCACTTGCTTCCGTTGAGGACAAAAGCCGCTGGTGGTAAAG | <u>83</u> |
| PMV_a0058 | GGTTTCGGATGTTACAGCGTCAGAAATCATAACGGGCAAACCTCA | <u>84</u> |
| PMV_a0059 | TCACTTGCTTCCGTTGAGGAAGAGTTATTGCTGGCGTTGTTGG | <u>85</u> |
| PMV_a0060 | GGTTTCGGATGTTACAGCGTGCCCGGCATTATTTTCATTGTTCTG | <u>86</u> |
| PMV_b0053 | TTGGGCTGGCGGTTTAGAGTTGA | <u>87</u> |
| PMV_b0054 | GTGCGACCGCCCTTGTTTATGG | <u>88</u> |
| PMV_b0055 | GCGTTGTTGGCCTTTTTCTTGTCT | <u>89</u> |
| PMV_b0056 | GCCCGGCATTATTTTCATTGTTCTG | <u>90</u> |
| PMV_b0057 | ACAAAAGCCGCTGGTGGTAAAG | <u>91</u> |
| PMV_b0058 | CAGAAATCATAACGGGCAAACCTCA | <u>92</u> |
| PMV_b0059 | AAGAGTTATTGCTGGCGTTGTTGG | <u>93</u> |
| PMV_b0060 | GCCCGGCATTATTTTCATTGTTCTG | <u>94</u> |

Please replace Table 6, beginning on page 9 and bridging to page 10, with a new Table 6 as follows:

Table 6. Exemplary HCoV-OC43 Primers

| Id | Sequence | SEQ ID NO: |
|---------------|---|------------|
| PMV_a0061 | TCACTTGCTTCCGTTGAGGTTGGGGTGATGGGTTTCAGATTA A | <u>95</u> |
| PMV_a0062 | GGTTTCGGATGTTACAGCGTCTCGGGAAGATCGCCTTCTTCTA | <u>96</u> |
| PMV_b006 1 | TTGGGGTGATGGGTTTCAGATTAA | <u>97</u> |
| PMV_b006 2 | CTCGGGAAGATCGCCTTCTTCTA | <u>98</u> |

Please replace Table 7, beginning on page 10 and bridging to page 11, with a new Table 7 as follows:

Table 7. Exemplary Influenza A Virus Probes

| Id | Sequence | SEQ ID NO: |
|------------|--|------------|
| PBIA_00001 | TTTAGAGCCTATGTGGATGGATTCTRAACCGAACGGCTGCATTGAGGGCAAGCT TTCTCAAATGTC | <u>99</u> |
| PBIA_00002 | ACAATTGAAGAAAGATTTGAAATCACTGGAACCATGCGCAGGCTTGCCGACCA AAGTCTCCCACCGAACT | <u>100</u> |
| PBIA_00003 | AGCAATNGAGGAGTGCCTGATTAANGATCCCTGGGTTTTGCTNAATGC | <u>101</u> |
| PBIA_00004 | CCATACAGCCATGGAACAGGAACAGGATACACCATGGACACAGTCAACAGAAC ACANCAATATTCAGAAA | <u>102</u> |
| PBIA_00005 | GGGCGGGGAGTCTTCGAGCTCTCNGACGAAAAGGCAACGAACCCGATCGTGCC | <u>103</u> |
| PBIA_00006 | GATCTNGAGGCTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTACCTCT GACTAA | <u>104</u> |

Please replace Table 8, beginning on page 11, with a new Table 8 as follows:

Table 8. Exemplary Influenza B Virus Probes

| Id | Sequence | SEQ ID NO: |
|------------|---|------------|
| PBIB_00001 | GCTGGGAAATAGCATGGAAGTATGATATTCAGCTACAATCAAGACTATTCGT TAAGTAATGAATCCTCA | <u>105</u> |
| PBIB_00002 | TCTGTTCCAGCTGGTTTCTCCAATTTTGAAGGAATGAGGAGCTACATAGACAA TATAGATCCTAAAGGAG | <u>106</u> |
| PBIB_00003 | TTACAACCATGAGCTACCAGAAGTTCATATAATGCCTTTCTTCTAATGTCTG ATGAATTGGGGCTGGCC | <u>107</u> |
| PBIB_00004 | ACAAATAAGATCCAAATGAAATGGGGAATGGAAGCTAGAAGATGTCTGCTTCA ATCAATGCAACAAATGG | <u>108</u> |
| PBIB_00005 | GAGGGAATGTATTCTGGAATAGANGAATGTATTAGTAACAACCCTTGGGTAAT ACAGAGTGCATACTGGT | <u>109</u> |
| PBIB_00006 | CTACCGTGTTGGGAGTAGCCGCACTAGGTATCAAAAACATTGGAAACAAAGAA TACTTATGGGATGGACT | <u>110</u> |
| PBIB_00007 | GGCTATGACTGAAAGAATAACCAGAGACAGCCCAATTTGGTTCCGGGATTTTT GTAGTATAGCACCGGTC | <u>111</u> |
| PBIB_00008 | ACTGATCAGAGGAACATGATTCTTGAGGAACAATGCTACGCTAAGTGTTGCAA CCTTTTGTAGGCCTGTT | <u>112</u> |
| PBIB_00009 | AAAATCCCTTTGTNGGACATTTGTCTATTGAGGGCATCAAAGANGCAGATATA ACCCAGCACATGGTCC | <u>113</u> |
| PBIB_00010 | CTTGGAATACAAGGGAATACAACCTTAAAACAAATGCTGAAGACATAGGAACCA AAGGCCAAATGTGCTCA | <u>114</u> |
| PBIB_00011 | GTGGCAGGAGCAACATCAGCTGAGTTCATAGAAATGCTACACTGCTTACAAGG TGAAAATTGGAGACAAA | <u>115</u> |
| PBIB_00012 | GGAACCCATCCCCGGAAGAGCAACCACAAGCAGTGAAGCTGATGTGCGAAGG AAAACCCAAAAGAAACA | <u>116</u> |
| PBIB_00013 | CTGTTTCCAAAGATCAAAGGCACTAAAAAGAGTTGGACTTGACCCTTCATTAA TCAGTACCTTTGCAGGA | <u>117</u> |
| PBIB_00014 | AGAGTTTTGTCTGCATTAACAGGCACAGAATTCAAGCCTAGATCAGCATTA ATGCAAGGGTTTCCATG | <u>118</u> |
| PBIB_00015 | GAGGGACGTGATGCAGATGTCAAAGGAAATCTACTCAAGATGATGAATGACTC AATGGCTAAGAAAACCA | <u>119</u> |
| PBIB_00016 | CCTATCAGGAATGGGAACAACAGCAACAAAAAGAAAGGCCTGATTCTAGCTG AGAGAAAAATGAGAAGA | <u>120</u> |
| PBIB_00017 | GCAAGTCAAAGAATGGGGAAGGAATTGCAAAGGATGTAATGGAAGTGCTAAA GCAGAGCTCTATGGGAA | <u>121</u> |

Please replace Table 9, beginning on page 11 and bridging to page 12, with a new Table 9 as follows:

Table 9. Exemplary Human Metapneumovirus Probes

| Id | Sequence | SEQ ID NO: |
|-----------|--|------------|
| PBM_00001 | AAAAGTGTATCACAGAAGTTTGTTCATTGAGTATGGCAAAGCATTAGGCTCAT CATCTACAGGCAGCAAA | <u>122</u> |
| PBM_00002 | GAAAGTCTATTTGTTAATATATTCATGCAAGCTTATGGAGCCGGTCAAACAAT GCTAAGGTGGGGGGTCA | <u>123</u> |
| PBM_00003 | ACGCTGTTGTGTGGAGAAATCTGTATGCTAAACATGCTGATTACAAATATGC TGCAGAAATAGGAATAC | <u>124</u> |
| PBM_00004 | TTAAGGAATCATCAGGTAATATCCCACAAAATCAGAGGCCCTCAGCACCAGAC ACACCCATAATCTTATT | <u>125</u> |
| PBM_00005 | TGAGCAATCAAAGGAGTGCAACATCAACATATCCACTACAAATTACCCATGCA AAGTCAGCACAGGAAGA | <u>126</u> |
| PBM_00006 | CTGTTCCATTGGCAGCAACAGAGTAGGGATCATCAAGCAGCTGAACAAAGGTT GCTCCTATATAACCAAC | <u>127</u> |
| PBM_00007 | ACTTAATGACAGATGCTGAACTAGCCAGGGCCGTTTCTAACATGCCGACATCT GCAGGACAAATAAAATT | <u>128</u> |
| PBM_00008 | AAAAAAGGGAAACTATGCTTGCCTCTTAAGAGAAGACCAAGGGTGGTATTGT CAGAATGCAGGGTCAAC | <u>129</u> |
| PBM_00009 | GAAAAGAACACACCAGTTACAATACCAGCATTTATCAAATCGGTTTCTATCAA AGAGAGTGAATCAGCCA | <u>130</u> |
| PBM_00010 | CAAATCAGTTGGCAAAAAACACATGATCTGATCGCATTATGTGATTTTATGG ATCTAGAAAAGAACACA | <u>131</u> |
| PBM_00011 | CAGCTAAAGACACTGACTATAACTACTCTGTATGCTGCATCACAAAGTGGTCC AATACTAAAAGTGAATG | <u>132</u> |
| PBM_00012 | AAAAGAACACACCAGTTACAATACCAGCATTTATCAAATCGGTTTCTATCAA GAGAGTGAATCAGCCAC | <u>133</u> |
| PBM_00013 | CTATTATAGGAGAAAAAGTGAACACTGTATCTGAAACATTGGAATTACCTACT ATCAGTAGACCCACCAA | <u>134</u> |
| PBM_00014 | AAGTTAGCATGGACAGACAAAGGTGGGGCAATCAAACTGAAGCAAAGCAAAC AATCAAAGTTATGGATC | <u>135</u> |
| PBM_00015 | CAGGAAAATACACAAAGTTGGAGAAAGATGCTCTAGACTTGCTTTCAGACAAT GAAGAAGAAGATGCAGA | <u>136</u> |
| PBM_00016 | CTAATAGCAGACATAATAAAGAAGCCAAGGGAAAAGCAGCAGAAATGATGGA AGAAGAAATGAACCAGC | <u>137</u> |

Please replace Table 10, beginning on page 12 and bridging to page 13, with a new Table 10 as follows:

Table 10. Exemplary Human Adenovirus Probes

| Id | Sequence | SEQ ID NO: |
|------------|---|------------|
| PBAd_00001 | CTGACACCTACCAAGGTATAAAATCAAACGGAAACGGTAATCCTCAAACTGG ACCAAAAATGACGATTT | <u>138</u> |
| PBAd_00002 | TCCTCTACTCCAACATTGCACTGTACCTGCCTGACAAGCTAAAATACACTCCT ACAAATGTGGAAATATC | <u>139</u> |
| PBAd_00003 | GCTATCGGAGGCAGAGTACTAAAAAGACTACTCCCATGAAACCATGCTACGG ATCGTATGCCAGACCTA | <u>140</u> |
| PBAd_00004 | AGTATTGTTTTGTACAGTGAGGATGTTAATATGGAACTCCTGATACTCACAT TTCATACAAACCAAGCA | <u>141</u> |
| PBAd_00005 | GGGAAACGATCTTAGAGTTGACGGGGCTAGCATTAAAGTTTGACAGCATTTGTC TTTACGCCACCTTCTTC | <u>142</u> |
| PBAd_00006 | TTGCCATTAAAAACCTCCTCCTCGCCAGGCTCATATACATATGAATGGAAC TTCAGGAAGGATGTTAA | <u>143</u> |
| PBAd_00007 | TTGCAACACGTAATGAAATAGGAGTGGGTAACAACCTTTGCCATGGAAATTAAC CTAAATGCCAACCTATG | <u>144</u> |
| PBAd_00008 | TTGGGGTAACTGACACCTATCAAGCTATTAAGGCTAATGGCAATGGCTCAGGC GATAATGGAGATATTAC | <u>145</u> |
| PBAd_00009 | AGGTATCAAGGCATTAAAGTTAAAACCGATGACGCTAATGGATGGGAAAAAGA TGCTAATGTTGATACAG | <u>146</u> |
| PBAd_00010 | GAGAAGTTTCTGTACTCCAATGTGGCTTTGTACCTTCCAGATGTTTACAAGT ACACGCCACCTAACATT | <u>147</u> |
| PBAd_00011 | ATCAGTCATTTAACGACTACCTCTCTGCAGCTAACATGCTTTACCCCATTCCT GCCAATGCAACCAACAT | <u>148</u> |
| PBAd_00012 | CTACTTCGTATATTCTGGATCTATTCCCTACCTGGATGGCACCTTTTACCTTA ACCACACTTTCAAGAAG | <u>149</u> |
| PBAd_00013 | ACCTGCCAGTGGAAGGATGCTAACAGCAAAATGCATACCTTTGGGGTAGCTGC CATGCCAGGTGTTACTG | <u>150</u> |
| PBAd_00014 | ATAGAAGCTGATGGGCTGCCTATTAGAATAGATTCAACTTCTGGAAGTGACAC AGTAATTTATGCTGATA | <u>151</u> |
| PBAd_00015 | TTGAAATTAAGCGCACCGTGGACGGCGAGGGGTACAACGTGGCCCAGTGCAAC ATGACCAAGGACTGGTT | <u>152</u> |
| PBAd_00016 | CGGCAACGACCGGCTCCTGACGCCCAACGAGTTTGAAATTAAGCGCACCGTGG ACGGCGAGGGGTACAAC | <u>153</u> |
| PBAd_00017 | CTCCAGTAACTTTATGTCCATGGGCGCACTCACAGACCTGGGCCAAAACCTTC | <u>154</u> |

| Id | Sequence | SEQ ID NO: |
|-------------------------|---|------------|
| | TCTACGCCAACTCCGCC | |
| PBA _d _00018 | GCTAACTTCCCCTATCCGCTTATAGGCAAGACCGCAGTTGACAGCATTACCCA GAAAAAGTTTCTTTGCG | <u>155</u> |
| PBA _d _00019 | ACAGTCCTTCCAACGTAAAAATTTCTGATAACCCAAACACCTACGACTACATG AACAAAGCGAGTGGTGGC | <u>156</u> |
| PBA _d _00020 | AAGATGAACTTCCAAATTACTGCTTTCCACTGGGAGGTGTGATTAATACAGAG ACTCTTACCAAGGTAAA | <u>157</u> |
| PBA _d _00021 | AGCTAACATGCTTTACCCCATCCCTGCCAATGCAACCAACATTCCAATTTCCA TCCCATCTCGCAACTGG | <u>158</u> |
| PBA _d _00022 | TTCAACTCTTGAAGCCATGCTGCGCAACGATACCAATGATCAGTCATTCAACG ACTACCTCTCTGCAGCT | <u>159</u> |
| PBA _d _00023 | AGGCTGTGGACAGCTATGATCCCGATGTTTCGTATTATTGAAAATCATGGCGTC GAGGATGAACTGCCTAA | <u>160</u> |
| PBA _d _00024 | TGAAATTGTGCTTTACACGGAAAATGTCAATTTGGAACTCCAGACAGCCATG TGGTATACAAGCCAGGA | <u>161</u> |
| PBA _d _00025 | CATCGGCTATCAGGGCTTCTACATTCCAGAAGGATACAAAGATCGCATGTATT CATTTTTTCAGAACTTC | <u>162</u> |
| PBA _d _00026 | GCTGCTTCTCCCAGGCTCCTACACTTATGAGTGGAACCTTTAGGAAGGATGTGA ACATGGTTCTACAGAGT | <u>163</u> |
| PBA _d _00027 | ATGACACCAATGATCAGTCATTCAACGACTACCTATCTGCAGCTAACATGCTC TACCCCATTCCTGCCAA | <u>164</u> |
| PBA _d _00028 | CTTGCCAACTACAACATTGGATACCAGGGCTTCTACGTTCCCTGAGGGTTACAA GGATCGCATGTACTCCT | <u>165</u> |
| PBA _d _00029 | GATCGCATGTACTCCTTCTTCAGAACTTCCAGCCCATGAGTAGACAGGTGGT TGATGAGATTAACCTACA | <u>166</u> |
| PBA _d _00030 | CCCCTAAGGGCGCTCCCAATACATCTCAGTGGATTGCTGAAGGCGTAAAAAAA GAAGATGGGGGATCTGA | <u>167</u> |
| PBA _d _00031 | AGAAAATGTAAATTTGGAACTCCAGATTCCCATGTTGTTTACAAAGCAGGAA CTTCAGACGAAAGCTCT | <u>168</u> |
| PBA _d _00032 | TGTGGCTACCAATACTGTTTACCAAGGTGTTAAGTTACAAACTGGTCAAACCTG ACAAATGGCAGAAAGAT | <u>169</u> |
| PBA _d _00033 | CCGAATTGGGAAGGGTAGCGTATTCGCCATGGAAATCAATCTCCAGGCCAAC TGTGGAAGAGTTTCTG | <u>170</u> |

| Id | Sequence | SEQ ID NO: |
|------------|--|-------------------|
| PBAd_00034 | TTGATGAGGTCAATTACAAAGACTTCAAGGCCGTCGCCATACCCTACCAACAC AACAACTCTGGCTTTGT | <u>171</u> |
| PBAd_00035 | TGACGAAGAGGAAGAGAAAAATCTCACCCTTACACTTTTGGAATGCCCCAG TGAAAGCAGAAGGTGGT | <u>172</u> |
| PBAd_00036 | AGAAGATTTTGACATTGACATGGCTTTCTTTGATTCCAACACTATTAACACAC CAGATGTTGTGCTGTAT | <u>173</u> |

Please replace Table 11, beginning on page 13 and bridging to page 14, with a new Table 11 as follows:

Table 11. Exemplary HCoV-OC229E Probes

| Id | Sequence | SEQ ID NO: |
|-----------|---|-------------------|
| PBS10049 | AATGGGGTTATGTTGGTTCCTCTCCACTAATCACCATGCAATTTGTAATGTTCA TAGAAATGAGCATGT | <u>174</u> |
| PBS10050 | GTGTATGACTGCTTTGTGAAGAATGTGGATTGGTCAATTACCTACCCTATGATAG CTAATGAAAATGCCA | <u>175</u> |
| PBS10051 | TTGCATCTTCTTTTGTGGTATGCCATCTTTTGTTCATATGAAACAGCAAGACA AGAGTATGAAAATGC | <u>176</u> |
| PBS10052 | AAATGGTTTCCTCACCACAAATAATCAAACAATTGAAGAAGGCTATGAATGTTGCA AAAGCTGAGTTTGAC | <u>177</u> |
| PBS10053 | CTGCTGCAGCTATGTACAAAGAAGCACGTGCTGTTAATAGAAAATCAAAAGTTGT TAGTGCCATGCATAG | <u>178</u> |
| PBS10054 | ACGTTTGGACATGTCTAGTGTGACACTATCCTTAATATGGCACGTAATGGTGT GTCCCTCTTTCCGTT | <u>179</u> |
| PBS10055 | CTGGTGGTAAAGTTTCATTTCTGATGACGTTGAAGTAAAGACATTGAACCTGT TTACAGAGTCAAGCT | <u>180</u> |
| PBS10056 | TTTACAGAGTCAAGCTTTGCTTTGAGTTTGAAGATGAAAACTTGTTAGATGTTTG TGAAAAGGCAATTGG | <u>181</u> |
| PBS10057 | GATGTTTGTGAAAAGGCAATTGGCAAGAAAATTAAACATGAAGGTGACTGGGATA GCTTTTGTAAGACTA | <u>182</u> |
| PBS10058 | GCGTTGTTGGCCTTTTCTTGTCTAAGCATAGTGATTTTGGTCTTGGTGATCTTG TCGATTCTTATTTTG | <u>183</u> |

| <u>Id</u> | <u>Sequence</u> | <u>SEQ ID NO:</u> |
|-----------|--|-------------------|
| PBS10059 | AGCAAGACAAGAGTATGAAAATGCTGTTGCAAATGGTTCCTCACCACAAATAATC AAACAATTGAAGAAG | <u>184</u> |
| PBS10060 | TTGAAGAAGGCTATGAATGTTGCAAAGCTGAGTTTGACAGGGAATCATCTGTTC AAAAGAAAATTAACA | <u>185</u> |
| PBS10061 | CTGCTGCAGCTATGTACAAAGAAGCACGTGCTGTTAATAGAAAATCAAAAGTTGT TAGTGCCATGCATAG | <u>186</u> |

Please replace Table 12, beginning on page 14, with a new Table 12 as follows:

Table 12. Exemplary HCoV-OC43 Probes

| <u>Id</u> | <u>Sequence</u> | <u>SEQ ID NO:</u> |
|-----------|--|-------------------|
| PBS10062 | CTCACATCCTAGGAAGATGCATAGTTTTAGATGTTAAAGGTGTAGAAGAATTGCATGACGATTTAGTTA A | <u>187</u> |
| PBS10063 | GGATTGGCCATTGCACCATAGCTCAACTCACGGATGCAGCACTGTCCATTAAGGAAAATGTTGATTTTA T | <u>188</u> |
| PBS10064 | GCATGCAATTCAATTATAAAATCACCATCAACCCCTCATCACGGCTAGACTTGAAATAGTTAAGCTCG G | <u>189</u> |
| PBS10065 | ATAGTTAGTCACTGGATGGGAATTCGTTTTGAATACACATCACCCACTGATAAGCTAGCTATGATTATG G | <u>190</u> |

Please replace Table 13, beginning on page 23 and bridging to page 24, with a new Table 13 as follows:

Table 13. Exemplary SARS-CoV probes

| <u>probe_id</u> | <u>Sequence 5'-3'</u> | <u>SEQ ID NO:</u> | <u>region</u> |
|-----------------|---|-------------------|--------------------------|
| PBS00001 | TTACCCTAATATGTTTATCACCCGCGAAGAAGCTATT CGTCACGTTTCGTGCGTGGA | <u>191</u> | SARS-Cov Replicase 1B |
| PBS00002 | CTGACAAGTATGTCCGCAATCTACAACACAGGCTCTA TGAGTGTCTCTATAGAAAT | <u>192</u> | SARS-Cov Replicase 1B |
| PBS00003 | CATAACACTTGCTGTAAC'TTATCACACCGTTTCTACA GGTTAGCTAACGAGTGTGC | <u>193</u> | SARS-Cov Replicase 1B |
| PBS00004 | TTACCCTAATATGTTTATCACCCGCGAAGAAGCTATT CGTCACGTTTCGTG | <u>194</u> | SARS-Cov Replicase 1B |
| PBS00009 | GCGTTCTCTTAAAGCTCCTGCCGTAGTGTCAAGTATCA TCACCAGATGCTGTTACTACATATAATGGATAC | <u>195</u> | SARS-Cov Replicase 1A |

| probe_id | Sequence 5'-3' | SEQ ID NO: | region |
|----------|---|------------|--------------------------|
| PBS00010 | CTTTGGCTGGCTCTTACAGAGATTGGTCCTATTTCAGG ACAGCGTACAGAGTTAGGTGTTGAATTTCTTAA | <u>196</u> | SARS-Cov Replicase 1A |
| PBS00011 | CTACGTAGTGAAGCTTTCGAGTACTACCATACTCTTG ATGAGAGTTTTCTTGGTAGGTACATGTCTGCTT | <u>197</u> | SARS-Cov Replicase 1A |
| PBS00012 | TGCCAATTGGTTATGTGACACATGGTTTTAATCTTGA AGAGGCTGCGCGCTGTATGCGTTCTCTTAAAGC | <u>198</u> | SARS-Cov Replicase 1A |
| PBS00013 | TATAAAGTTACCAAGGGAAAGCCCGTAAAAGGTGCTT GGAACATTGGACAACAGAGATCAGTTTTAACAC | <u>199</u> | SARS-Cov Replicase 1A |
| PBS00014 | TGCTTCATTGATGTTGTTAACAAGGCACTCGAAATGT GCATTGATCAAGTCACATATCGCTGGCGCAAAG | <u>200</u> | SARS-Cov Replicase 1A |
| PBS00015 | TGTCGACGCCATGGTTTATACTTCAGACCTGCTCACC AACAGTGTCAATTATTATGGCATATGTAAGTGGT | <u>201</u> | SARS-Cov Replicase 1A |
| PBS00016 | TACTGTTGAAAACTCAGGCCTATCTTTGAATGGATT GAGGCGAACTTAGTGCAGGAGTTGAATTTCTC | <u>202</u> | SARS-Cov Replicase 1A |
| PBS00017 | ACCTATTCTGTTGCTTGACCAAGCTCTTGTATCAGAC GTTGGAGATAGTACTGAAGTTTCC | <u>203</u> | SARS-Cov Replicase 1A |
| PBS00018 | GCCTATTAATGTCATAGTTTTTGATGGCAAGTCCAAA TGCGACGAGTCTGCTTCTAAGTCTGCTTCTGTG | <u>204</u> | SARS-Cov Replicase 1A |
| PBS00019 | TGAGAGCTAACAACACTAAAGGTTCACTGCCTATTAA TGTCATAGTTTTTGATGGCAAGTCCAAATGCGA | <u>205</u> | SARS-Cov Replicase 1A |
| PBS00020 | ACTTGCATGATGTGCTATAAGCGCAATCGTGCCACAC GCGTTGAGTGTACAACATTTGTTAATGGCATGA | <u>206</u> | SARS-Cov Replicase 1A |
| PBS00021 | GGCGATGTAGTGGCTATTGACTATAGACACTATTTCAG CGAGTTTCAAGAAAGGTGCTAAATTACTGCATA | <u>207</u> | SARS-Cov Replicase 1A |
| PBS00022 | TCAAACCAAACACTTGGTGTTTACGTTGTCTTTGGAG TACAAAGCCAGTAGATACTTCAAATTCATTTGA | <u>208</u> | SARS-Cov Replicase 1A |
| PBS00023 | TAGTGCTGTTGGCAACATTTGCTACACACCTTCCAAA CTCATTGAGTATAGTGATTTTGCTAC | <u>209</u> | SARS-Cov Replicase 1A |
| PBS00024 | TCATAGCTAACATCTTTACTCCTCTTGTGCAACCTGT GGGTGCTTTAGATGTGTCTGCTTCAGTAGTGGC | <u>210</u> | SARS-Cov Replicase 1A |
| PBS00025 | GGTATTATTGCCATATTGGTGACTTGTGCTGCCTACT ACTTTATGAAATTCAGACGTGTTTTTGGTGAGT | <u>211</u> | SARS-Cov Replicase 1A |
| PBS00026 | GTGATGTCAGAGAACTATGACCCATCTTCTACAGCA TGCTAATTTGGAATCTGCAAAGCGAGTTCTTAA | <u>212</u> | SARS-Cov Replicase 1A |
| PBS00027 | AACCATCAAGCCTGTGTCGTATAAACTCGATGGAGTT ACTTACACAGAGATTGAACCAAATTTGGATGGG | <u>213</u> | SARS-Cov Replicase 1A |

| probe_id | Sequence 5'-3' | SEQ ID NO: | region |
|----------|--|------------|-------------------------------------|
| PBS00028 | GTTTTCTACAAGGAAACATCTTACACTACAACCATCA AGCCTGTGTCGTATAAACTCGATGGAGTTACTT | <u>214</u> | SARS-Cov Replicase 1A |
| PBS00029 | CCTTGAATGAGGATCTCCTTGAGATACTGAGTCGTGA ACGTGTTAACATTAACATTGTTGGCGATTTTCA | <u>215</u> | SARS-Cov Replicase 1A |
| PBS00031 | GCCATGGTTTTATACTTCAGACCTGCTCACCAACAGTG TCATTATTATGGCATATGTAACCTGGTGGTCTTG | <u>216</u> | SARS-Cov Replicase 1A |
| PBS00032 | CAACAGACTTCTCAGTGGTTGTCTAATCTTTGGGCA CTACTGTTGAAAACTCAGGCCTATCTTTGAAT | <u>217</u> | SARS-Cov Replicase 1A |
| PBS00033 | TTCCCGTCAGGCAAAGTTGAAGGGTGCATGGTACAAG TAACCTGTGGAAC TACAAC | <u>218</u> | SARS-Cov Replicase 1A |
| PBS00034 | GGTTCACCATCTGGTGT TTTATCAGTGTGCCATGAGAC CTAATCATAACCATTAAGG | <u>219</u> | SARS-Cov Replicase 1A |
| PBS00035 | AGATCATGTTGACATATTGGGACCTCTTTCTGCTCAA ACAGGAATTGCCGTC | <u>220</u> | SARS-Cov Replicase 1A |
| PBS00036 | TAAAAAGGACAAAAAGAAAAAGACTGATGAAGCTCAG CCTTTGCCGCAGAGACAAAAGAAGCAGCCCACT | <u>221</u> | SARS-Cov Nucleocapsid gene |
| PBS00037 | ACGGCAAAATGAAAGAGCTCAGCCCCAGATGGTACTT CTATTACCTAGGAAC TGGCCAGAAAGCTTCACT | <u>222</u> | SARS-Cov Nucleocapsid gene |
| PBS00038 | GGCGCTAACAAAAGAAGGCATCGTATGGGTTGCAACTG AGGGAGCCTTGAATACACCCAAAGACCACATTG | <u>223</u> | SARS-Cov Nucleocapsid gene |
| PBS00039 | GTCCAGATGACCAAATTTGGCTACTACCGAAGAGCTAC CCGACGAGTTCTGTGGTGGTGACGGCAAAATGAA | <u>224</u> | SARS-Cov Nucleocapsid gene |
| PBS00040 | GAGGTGGTGAAACTGCCCTCGCGCTATTGCTGCTAGA CAGATTGAACCAGCTTGAGAGCAAAGTTTCTGG | <u>225</u> | SARS-Cov Nucleocapsid gene |
| PBS00041 | AAAAGAAAAAGACTGATGAAGCTCAGCCTTTGCCGCA GAGACAAAAGAAGCAGCCCACTGTGACTCTTCT | <u>226</u> | SARS-Cov Nucleocapsid gene |
| PBS00042 | AAATTGCACAATTTGCTCCAAGTGCCTCTGCATTCTT TGGAATGTCACGCATTGGCATGGAAGTCACACC | <u>227</u> | SARS-Cov Nucleocapsid gene |
| PBS00043 | ACCAATTTAACAAGGCGATTAGTCAAATTTCAAGAATC ACTTACAACAACATCAACTGCATTGGGCAAGCT | <u>228</u> | SARS-Cov Spike glycoprotein gene |
| PBS00044 | CACCTGGAACAAATGCTTCATCTGAAGTTGCTGTTCT ATATCAAGATGTTAACTGCACTGATGTTTCTAC | <u>229</u> | SARS-Cov Spike glycoprotein gene |
| PBS00045 | AAAGGGCTACCACCTTATGTCCTTCCCACAAGCAGCC CCGCATGGTGTGTCTTCCTACATGTCACGTAT | <u>230</u> | SARS-Cov Spike glycoprotein gene |

| probe_id | Sequence 5'-3' | SEQ ID NO: | region |
|----------|---|------------|-------------------------------------|
| PBS00046 | TCAGGAAATTGTGATGTCGTTATTGGCATCATTAAACA ACACAGTTTATGATCCTCTGCAACCTGAGCTTG | <u>231</u> | SARS-Cov Spike glycoprotein gene |
| PBS00047 | TTGATCTTGGCGACATTTTCAGGCATTAACGCTTCTGT CGTCAACATTCAAAAAGAAATTGACCGCCTCAA | <u>232</u> | SARS-Cov Spike glycoprotein gene |
| PBS00048 | GAGGAACTTCACCACAGCGCCAGCAATTTGTCATGAA GGCAAAGCATACTTCCCTCGTGAAGGTGTTTTT | <u>233</u> | SARS-Cov Spike glycoprotein gene |

Please replace Table 15, beginning on page 28 and bridging to page 38, with a new Table 15 as follows:

Table 15. Exemplary probes for non-SARS-CoV infectious organisms causing SARS-like symptoms

| seqid | sequence (5'-3') | SEQ ID NO: | species |
|------------|---|------------|----------------------|
| PBIA_00001 | TTTAGAGCCTATGTGGATGGATTTCRAACCGAACGGC TGCATTGAGGGCAAGCTTTCTCAAATGTC | <u>234</u> | Influenza A virus |
| PBIA_00002 | ACAATTGAAGAAAGATTTGAAATCACTGGAACCATG CGCAGGCTTGCCGACCAAAGTCTCCCACCGAACT | <u>235</u> | Influenza A virus |
| PBIA_00003 | AGCAATNGAGGAGTGCCTGATTAANGATCCCTGGGT TTTGCTNAATGC | <u>236</u> | Influenza A virus |
| PBIA_00004 | CCATACAGCCATGGAACAGGAACAGGATACACCATG GACACAGTCAACAGAACACANCAATATTCAGAAA | <u>237</u> | Influenza A virus |
| PBIA_00005 | GGGCGGGGAGTCTTCGAGCTCTCNGACGAAAAGGCA ACGAACCCGATCGTGCC | <u>238</u> | Influenza A virus |
| PBIA_00006 | GATCTNGAGGCTCTCATGGAATGGCTAAAGACAAGA CCAATCCTGTACCTCTGACTAA | <u>239</u> | Influenza A virus |
| PBIB_00001 | GCTGGGAAATAGCATGGAACGATGATATTCAGCTA CAATCAAGACTATTTCGTTAAGTAATGAATCCTCA | <u>240</u> | Influenza B virus |
| PBIB_00002 | TCTGTTCCAGCTGGTTTCTCCAATTTTGAAGGAATG AGGAGCTACATAGACAATATAGATCCTAAAGGAG | <u>241</u> | Influenza B virus |
| PBIB_00003 | TTACAACCATGAGCTACCAGAAGTTCCATATAATGC CTTCTTCTAATGTCTGATGAATTGGGGCTGGCC | <u>242</u> | Influenza B virus |
| PBIB_00004 | ACAAATAAGATCCAAATGAAATGGGGAATGGAAGCT AGAAGATGTCTGCTTCAATCAATGCAACAAATGG | <u>243</u> | Influenza B virus |
| PBIB_00005 | GAGGGAATGTATTCTGGAATAGANGAATGTATTAGT AACAAACCCTTGGGTAATACAGAGTGCATACTGGT | <u>244</u> | Influenza B virus |
| PBIB_00006 | CTACCGTGTGGGAGTAGCCGCACTAGGTATCAAAA ACATTGGAAACAAAGAATACTTATGGGATGGACT | <u>245</u> | Influenza B virus |

| seqid | sequence (5'-3') | SEQ ID NO: | species |
|------------|---|------------|----------------------|
| PBIB_00007 | GGCTATGACTGAAAGAATAACCAGAGACAGCCCAAT TTGGTTCCGGGATTTTTGTAGTATAGCACCGGTC | <u>246</u> | Influenza B virus |
| PBIB_00008 | ACTGATCAGAGGAACATGATTCTTGAGGAACAATGC TACGCTAAGTGTGCAACCTTTTTGAGGCCTGTT | <u>247</u> | Influenza B virus |
| PBIB_00009 | AAAATCCCTTTGTNGGACATTTGTCTATTGAGGGCA TCAAAGANGCAGATATAACCCCAGCACATGGTCC | <u>248</u> | Influenza B virus |
| PBIB_00010 | CTTGGAATACAAGGGAATACAACCTAAAACAAATGC TGAAGACATAGGAACCAAAGGCCAAATGTGCTCA | <u>249</u> | Influenza B virus |
| PBIB_00011 | GTGGCAGGAGCAACATCAGCTGAGTTCATAGAAATG CTACACTGCTTACAAGGTGAAAATTGGAGACAAA | <u>250</u> | Influenza B virus |
| PBIB_00012 | GGAACCCATCCCCGAAAGAGCAACCACAAGCAGTG AAGCTGATGTCGGAAGGAAAACCCAAAAGAAACA | <u>251</u> | Influenza B virus |
| PBIB_00013 | CTGTTTCCAAAGATCAAAGGCACTAAAAAGAGTTGG ACTTGACCCTTCATTAATCAGTACCTTTGCAGGA | <u>252</u> | Influenza B virus |
| PBIB_00014 | AGAGTTTTGTCTGCATTAACAGGCACAGAATTCAAG CCTAGATCAGCATTAATGCAAGGGTTTCCATG | <u>253</u> | Influenza B virus |
| PBIB_00015 | GAGGGACGTGATGCAGATGTCAAAGGAAATCTACTC AAGATGATGAATGACTCAATGGCTAAGAAAACCA | <u>254</u> | Influenza B virus |
| PBIB_00016 | CCTATCAGGAATGGGAACAACAGCAACAAAAAAGAA AGGCCGTATTCTAGCTGAGAGAAAAATGAGAAGA | <u>255</u> | Influenza B virus |
| PBIB_00017 | GCAAGTCAAAGAATGGGGAAGGAATTGCAAAGGAT GTAATGGAAGTGCTAAAGCAGAGCTCTATGGGAA | <u>256</u> | Influenza B virus |
| PBAd_00001 | CTGACACCTACCAAGGTATAAAATCAAACGGAAAACG GTAATCCTCAAACTGGACCAAAAATGACGATTT | <u>257</u> | Human adenovirus |
| PBAd_00002 | TCCTCTACTCCAACATTGCACTGTACCTGCCTGACA AGCTAAAATACACTCCTACAAATGTGGAAATATC | <u>258</u> | Human adenovirus |
| PBAd_00003 | GCTATCGGAGGCAGAGTACTAAAAAAGACTACTCCC ATGAAACCATGCTACGGATCGTATGCCAGACCTA | <u>259</u> | Human adenovirus |
| PBAd_00004 | AGTATTGTTTTGTACAGTGAGGATGTTAATATGGAA ACTCCTGATACTCACATTTTCATACAAACCAAGCA | <u>260</u> | Human adenovirus |
| PBAd_00005 | GGGAAACGATCTTAGAGTTGACGGGGCTAGCATTAA GTTTGACAGCATTTGTCTTTACGCCACCTTCTTC | <u>261</u> | Human adenovirus |
| PBAd_00006 | TTGCCATTAAAAACCTCCTCCTCCTGCCAGGCTCAT ATACATATGAATGGAACCTCAGGAAGGATGTTAA | <u>262</u> | Human adenovirus |
| PBAd_00007 | TTGCAACACGTAATGAAATAGGAGTGGGTAACAACT TTGCCATGGAAATTAACCTAAATGCCAACCTATG | <u>263</u> | Human adenovirus |

| seqid | sequence(5'-3') | SEQ ID NO: | species |
|------------|---|------------|---------------------|
| PBAd_00008 | TTGGGGTAAC TGACACCTATCAAGCTATTAAGGCTA ATGGCAATGGCTCAGGCGATAATGGAGATATTAC | <u>264</u> | Human adenovirus |
| PBAd_00009 | AGGTATCAAGGCATTAAAGTTAAAACCGATGACGCT AATGGATGGGAAAAGATGCTAATGTTGATACAG | <u>265</u> | Human adenovirus |
| PBAd_00010 | GAGAAGTTTTCTGTACTCCAATGTGGCTTTGTACCT TCCAGATGTTTACAAGTACACGCCACCTAACATT | <u>266</u> | Human adenovirus |
| PBAd_00011 | ATCAGTCATTTAACGACTACCTCTCTGCAGCTAACA TGCTTTACCCCATTCCTGCCAATGCAACCAACAT | <u>267</u> | Human adenovirus |
| PBAd_00012 | CTACTTCGTATATTCTGGATCTATTCCCTACCTGGA TGGCACCTTTTACCTTAACCACACTTTCAAGAAG | <u>268</u> | Human adenovirus |
| PBAd_00013 | ACCTGCCAGTGGAAAGGATGCTAACAGCAAAATGCAT ACCTTTGGGGTAGCTGCCATGCCAGGTGTTACTG | <u>269</u> | Human adenovirus |
| PBAd_00014 | ATAGAAGCTGATGGGCTGCCTATTAGAATAGATTCA ACTTCTGGAAC TGACACAGTAATTTATGCTGATA | <u>270</u> | Human adenovirus |
| PBAd_00015 | TTGAAATTAAGCGCACCGTGGACGGCGAGGGGTACA ACGTGGCCAGTGCAACATGACCAAGGACTGGTT | <u>271</u> | Human adenovirus |
| PBAd_00016 | CGGCAACGACCGGCTCCTGACGCCCAACGAGTTTGA AATTAAGCGCACCGTGGACGGCGAGGGGTACAAC | <u>272</u> | Human adenovirus |
| PBAd_00017 | CTCCAGTAAC TTTATGTCCATGGGCGCACTCACAGA CCTGGGCCAAAACCTTCTCTACGCCAACTCCGCC | <u>273</u> | Human adenovirus |
| PBAd_00018 | GCTAACTTCCCTATCCGCTTATAGGCAAGACCGCA GTTGACAGCATTACCCAGAAAAAGTTCTTTGCG | <u>274</u> | Human adenovirus |
| PBAd_00019 | ACAGTCCTTCCAACGTAAAAATTTCTGATAACCCAA ACACCTACGACTACATGAACAAGCGAGTGGTGGC | <u>275</u> | Human adenovirus |
| PBAd_00020 | AAGATGAACTTCCAAATTACTGCTTTCCACTGGGAG GTGTGATTAATACAGAGACTCTTACCAAGGTAAA | <u>276</u> | Human adenovirus |
| PBAd_00021 | AGCTAACATGC TTTACCCCATCCCTGCCAATGCAAC CAACATTCCAATTTCCATCCCATCTCGCAACTGG | <u>277</u> | Human adenovirus |
| PBAd_00022 | TTCAACTCTTGAAGCCATGCTGCGCAACGATACCAA TGATCAGTCATTCAACGACTACCTCTCTGCAGCT | <u>278</u> | Human adenovirus |
| PBAd_00023 | AGGCTGTGGACAGCTATGATCCCGATGTTTCGTATTA TTGAAAATCATGGCGTCGAGGATGAACTGCCATA | <u>279</u> | Human adenovirus |
| PBAd_00024 | TGAAATTGTGCTTTACACGGAAAATGTCAATTTGGA AACTCCAGACAGCCATGTGGTATACAAGCCAGGA | <u>280</u> | Human adenovirus |
| PBAd_00025 | CATCGGCTATCAGGGCTTCTACATTCCAGAAGGATA CAAAGATCGCATGTATTTCATTTTTCAGAACTTC | <u>281</u> | Human adenovirus |

| seqid | sequence (5' - 3') | SEQ ID NO: | species |
|------------|---|------------|---------------------|
| PBAd_00026 | GCTGCTTCTCCCAGGCTCCTACACTTATGAGTGGAA CTTTAGGAAGGATGTGAACATGGTTCTACAGAGT | <u>282</u> | Human adenovirus |
| PBAd_00027 | ATGACACCAATGATCAGTCATTCAACGACTACCTAT CTGCAGCTAACATGCTCTACCCCATTCCTGCCAA | <u>283</u> | Human adenovirus |
| PBAd_00028 | CTTGCCAACTACAACATTGGATACCAGGGCTTCTAC GTTCTTGAGGGTTACAAGGATCGCATGTACTCCT | <u>284</u> | Human adenovirus |
| PBAd_00029 | GATCGCATGTACTCCTTCTTCAGAACTTCCAGCCC ATGAGTAGACAGGTGGTTGATGAGATTAACATA | <u>285</u> | Human adenovirus |
| PBAd_00030 | CCCCTAAGGGCGCTCCCAATACATCTCAGTGGATTG CTGAAGGCGTAAAAAAGAAGATGGGGGATCTGA | <u>286</u> | Human adenovirus |
| PBAd_00031 | AGAAAAATGTAAATTTGGAACTCCAGATTCCCATGT TGTTTACAAAGCAGGAACCTTCAGACGAAAGCTCT | <u>287</u> | Human adenovirus |
| PBAd_00032 | TGTGGCTACCAATACTGTTTACCAAGGTGTTAAGTT ACAACTGGTCAAACCTGACAAATGGCAGAAAGAT | <u>288</u> | Human adenovirus |
| PBAd_00033 | CCGAATTGGGAAGGGTAGCGTATTCGCCATGGAAAT CAATCTCCAGGCCAACCTGTGGAAGAGTTTCTG | <u>289</u> | Human adenovirus |
| PBAd_00034 | TTGATGAGGTCAATTACAAAGACTTCAAGGCCGTCG CCATACCCTACCAACACAACACTCTGGCTTTGT | <u>290</u> | Human adenovirus |
| PBAd_00035 | TGACGAAGAGGAAGAGAAAAATCTCACCCTTACAC TTTGGAAATGCCCCAGTGAAAGCAGAAGGTGGT | <u>291</u> | Human adenovirus |
| PBAd_00036 | AGAAGATTTTGACATTGACATGGCTTTCTTTGATT CAACACTATTAAACACACCAGATGTTGTGCTGTAT | <u>292</u> | Human adenovirus |
| PBS10062 | CTCACATCCTAGGAAGATGCATAGTTTTAGATGTTA AAGGTGTAGAAGAATTGCATGACGATTTAGTTAA | <u>293</u> | HCoV-OC43 |
| PBS10063 | GGATTGGCCATTGCACCATAGCTCAACTCACGGATG CAGCACTGTCCATTAAAGGAAAATGTTGATTTTAT | <u>294</u> | HCoV-OC43 |
| PBS10064 | GCATGCAATTCAATTATAAAATCACCATCAACCCCT CATCACCGGCTAGACTTGAAATAGTTAAGCTCGG | <u>295</u> | HCoV-OC43 |
| PBS10065 | ATAGTTAGTCACTGGATGGGAATTCGTTTTGAATAC ACATCACCCACTGATAAGCTAGCTATGATTATGG | <u>296</u> | HCoV-OC43 |
| PBS10049 | AATGGGGTTATGTTGGTTCACTCTCCACTAATCACC ATGCAATTTGTAATGTTTCATAGAAATGAGCATGT | <u>297</u> | HCoV-229E |
| PBS10050 | GTGTATGACTGCTTTGTTAAGAATGTGGATTGGTCA ATTACCTACCCATGATAGCTAATGAAAATGCCA | <u>298</u> | HCoV-229E |
| PBS10051 | TTGCATCTTCTTTTGTGGTATGCCATCTTTTGTG CATATGAAACAGCAAGACAAGAGTATGAAAATGC | <u>299</u> | HCoV-229E |

| seqid | sequence(5'-3') | SEQ ID NO: | species |
|------------|---|------------|-------------------------------|
| PBS10052 | AAATGGTTCCTCACCACAAATAATCAAACAATTGAA GAAGGCTATGAATGTTGCAAAAGCTGAGTTTGAC | <u>300</u> | HCoV-229E |
| PBS10053 | CTGCTGCAGCTATGTACAAAGAAGCACGTGCTGTTA ATAGAAAATCAAAGTTGTTAGTGCCATGCATAG | <u>301</u> | HCoV-229E |
| PBS10054 | ACGTTTGGACATGTCTAGTGTGACACTATCCTTAA TATGGCACGTAATGGTGTGTCCCTCTTTCCGTT | <u>302</u> | HCoV-229E |
| PBS10055 | CTGGTGGTAAAGTTTCATTTTCTGATGACGTTGAAG TAAAAGACATTGAACCTGTTTACAGAGTCAAGCT | <u>303</u> | HCoV-229E |
| PBS10056 | TTTACAGAGTCAAGCTTTGCTTTGAGTTTGAAGATG AAAACTTGTAGATGTTTGTGAAAAGGCAATTGG | <u>304</u> | HCoV-229E |
| PBS10057 | GATGTTTGTGAAAAGGCAATTGGCAAGAAAATTAAA CATGAAGGTGACTGGGATAGCTTTTGTAAAGACTA | <u>305</u> | HCoV-229E |
| PBS10058 | GCGTTGTTGGCCTTTTTCTTGTCTAAGCATAGTGAT TTTGGTCTTGGTGATCTTGTGCGATTCTTATTTTG | <u>306</u> | HCoV-229E |
| PBS10059 | AGCAAGACAAGAGTATGAAAATGCTGTTGCAAATGG TTCCTCACCACAAATAATCAAACAATTGAAGAAG | <u>307</u> | HCoV-229E |
| PBS10060 | TTGAAGAAGGCTATGAATGTTGCAAAAGCTGAGTTT GACAGGGAATCATCTGTTCAAAGAAAATTAAACA | <u>308</u> | HCoV-229E |
| PBS10061 | CTGCTGCAGCTATGTACAAAGAAGCACGTGCTGTTA ATAGAAAATCAAAGTTGTTAGTGCCATGCATAG | <u>309</u> | HCoV-229E |
| PBHE_00001 | CGGGATAAGGCACTCTCTATCAGAATGGATGTCTTG CTGCTATAATAGATAGAGAAGGTTATAGCAGACT | <u>310</u> | Human enteric coronaviruse |
| PBHE_00002 | CCCTCGCAGGAAAGTCGGGATAAGGCACTCTCTATC AGAATGGATGTCTTGCTGCTATAATAGATAGAGA | <u>311</u> | Human enteric coronaviruse |
| PBHE_00003 | ATGGATGTTTGGAGACGCAGAGGAGAAGTTGGACAA CCCTAGTAGTTCAGAGGTGGATATAGTATGCT | <u>312</u> | Human enteric coronaviruse |
| PBHE_00004 | CCTTGGGTATGTACTTGCGTAAGTGTGGCGAAAAG GGTGCCCTACAATAAAGATCATAAACGTGTCCG | <u>313</u> | Human enteric coronaviruse |
| PBHE_00005 | GGGGATGCTGGTTTTACTAGCATACTCAGTGGTTTG TTATATGATTCACCTGTTTTTCACAGCAAGG | <u>314</u> | Human enteric coronaviruse |
| PBHE_00006 | CATGACGGCAGTTGCTTGTCAACCCCCGTACTGTTA TTTTTCGTAATTCTACTACCAACTATGTTGGTG | <u>315</u> | Human enteric coronaviruse |
| PBRh_00001 | GGCTGAGTGATTACATCAGGTTTGGGTAGAGCTT TTGGTGTCCGGTTCCTGACCAAATCTCAACAAA | <u>316</u> | Human rhinovirus |
| PBRh_00002 | GAAAAGCTATTAGCTTGGTAGACAGAACTACCAACG TTAGGTATAGTGTGGATCAACTGGTCACGGCTAT | <u>317</u> | Human rhinovirus |

| seqid | sequence (5'-3') | SEQ ID NO: | species |
|------------|---|------------|--------------------------|
| PBRh_00003 | GGCCAAGTAATAGCTAGACATAAGGTTAGGGAGTTT AACATAAATCCAGTCAACACGGCAACTAAGTCAA | <u>318</u> | Human rhinovirus |
| PBRh_00004 | GATAACAAGGGCATGTTATTACACAGTAATTTTGTT CTAGCCTCCACAAATTCTAACACACTAAGCCCCC | <u>319</u> | Human rhinovirus |
| PBRh_00005 | GGCCAAGAAGTAAGGTTGTGTTTAGTACCACTCAGG GTTTACCAGTTATGTTAACACCTGGATCTGGGCA | <u>320</u> | Human rhinovirus |
| PBRh_00006 | GTAATGCGTAAGTGCGGGATGGGACCAACTACTTTG GGTGTCCGTGTTTCCTGTTTTCTTTTGATTGCA | <u>321</u> | Human rhinovirus |
| PBRh_00007 | TAAAAGAGGATTCAGAGCTGATGAGCGCCACTCTTT CCTTATACACCCTACCTTTCTGTGGCTGAGATT | <u>322</u> | Human rhinovirus |
| PBRh_00008 | GCAAGTTTCATCAGGGTTTATTAATAGTTGCCGCCA TCCCAGAACATCAATTGGCATCTGCAACAAGTGG | <u>323</u> | Human rhinovirus |
| PBMP_00001 | ATATATGAAGGAACACCAGTGGCGAAGGCGAAAAC TAGGCCATTACTGACGCTTAGGCTTGAAAGTGTG | <u>324</u> | Mycoplasma pneumoniae |
| PBMP_00002 | GCAGTAGGGAATTTTTCACAATGAGCGAAAGCTTGA TGGAGCAATGCCGCGTGAACGATGAAGGTCTTTA | <u>325</u> | Mycoplasma pneumoniae |
| PBMP_00003 | AACACATTAAGTATCTCGCCTGGGTAGTACATTCGC AAGAATGAAACTCAAACGGAATTGACGGGGACCC | <u>326</u> | Mycoplasma pneumoniae |
| PBMP_00004 | ACACCGTAAACGATAGATACTAGCTGTCTGGGGCGAT CCCCTCGGTAGTGAAGTTAACACATTAAGTATCT | <u>327</u> | Mycoplasma pneumoniae |
| PBMP_00005 | ACATCCTTGGCAAAGTTATGGAACATAATGGAGGT TAACCGAGTGACAGGTGGTGCATGGTTGTCGTCA | <u>328</u> | Mycoplasma pneumoniae |
| PBR_00001 | TTATAACTTAACCGTCGGCAGTTGGGTAAAGAGACCA CGTCCGATCAATTGTCTGAGGGCGCGTGGAAGTG | <u>329</u> | Rubella virus |
| PBR_00002 | ATACCCAGACCTGTGTTTACGCAGATGCAGGTCAGT GATCACCCAGCACTCCACGCAATTTCTCGCGTATA | <u>330</u> | Rubella virus |
| PBR_00003 | AGAAACTCCTAGATGAGGTTCTTGCCCCCGGTGGGC CTTATAACTTAACCGTCGGCAGTTGGGTAAAGAGA | <u>331</u> | Rubella virus |
| PBR_00004 | ATACCCAGACCTGTGTTTACGCAGATGCAGGTCAGT GATCACCCAGCACTCCACGCAATTTCTCGCGTATA | <u>332</u> | Rubella virus |
| PBR_00005 | TCTTACTTCAACCCTGGCGGCAGCTACTACAAGCAG TACCACCCTACCGCGTGCGAGGTTGAACCT | <u>333</u> | Rubella virus |
| PBM_00001 | AAGGCTTGTTTTCAGAGATTGCAATGCATACTACTGA GGACAGGATCAGTAGAGCAGTTGGACCCAGACAA | <u>334</u> | Measles virus |
| PBM_00002 | AGGATCAGTAGAGCAGTTGGACCCAGACAAGCCCAA GTGTCAATTCCTACACGGTGATCAAAGTGAGAATG | <u>335</u> | Measles virus |

| seqid | sequence (5' - 3') | SEQ ID NO: | species |
|-------------|--|------------|---|
| PBM_00003 | TCAGTAGAGCAGTTGGACCCAGACAAGCCCAAGTGT CATTCCTACACGGTGATCAAAGTGAGAATG | <u>336</u> | Measles virus |
| PBM_00004 | CCCAGGGAATGTACGGGGGAACCTACCTAGTTGAAA AGCCTAATCTGAGCAGCAAAGGATCAGAATTATC | <u>337</u> | Measles virus |
| PBM_00005 | CCCAGGGAATGTACGGGGGAACCTACCTAGTTGAAA AGCCTAATCTGAGCAGCAAAGGATCAGAATTATC | <u>338</u> | Measles virus |
| PBRSV_00001 | CAAACCCACAAACAAACCAACCACCAAAACCACAAA CAAAAGAGACCCAAAAACACCAGCCAAAACGACG | <u>339</u> | Human respiratory syncytial virus |
| PBRSV_00002 | GCAGCACTTGTAATAACCAAATTAGCAGCAGGAGAC AGATCAGGTCTTACAGCAGTAATTAGGAGGGCAA | <u>340</u> | Human respiratory syncytial virus |
| PBRSV_00003 | CAAGAGGGGGTAGTAGAGTTGAAGGAATCTTTGCAG GATTGTTTATGAATGCCTATGGTTCAGGGCAAGT | <u>341</u> | Human respiratory syncytial virus |
| PBRSV_00004 | GACTTAACAGCAGAAGAATTGGAAGCCATAAAGAAT CAACTCAACCCTAAAGAAGATGATGTAGAGCTTT | <u>342</u> | Human respiratory syncytial virus |
| PBRSV_00005 | TCACAATCCACTGTGCTCGACACAACCACATTAGAA CACACAATCCAACAGCAATCCCTCCACTCAACCA | <u>343</u> | Human respiratory syncytial virus |
| PBRSV_00006 | GACTTAACAGCAGAAGAATTGGAAGCCATAAAGAAT CAACTCAACCCTAAAGAAGATGATGTAGAGCTTT | <u>344</u> | Human respiratory syncytial virus |
| PBPI_00001 | GCCGACGACCATCAAGCGTAGCCAAACAAGATCAGA GAGAACACAGAATTCAGAACTCCACAAATCAACA | <u>345</u> | Parainfluenza |
| PBPI_00002 | CGACCCAAGATCATAGATCAAGTGAGGAGAGTGGA TCTCTAGGAGAACAGGTGAGTCAAAAAC TGAGAC | <u>346</u> | Parainfluenza |
| PBPI_00003 | CGCAATGAAGAGGGAACCAGCAACACATCAGTCGA TGAGATGGCCAAGTTACTAGTAAGTCTTGGTGTA | <u>347</u> | Parainfluenza |
| PBPI_00004 | CTCCTTGCAATGGCCATACGTAGTCCGGAATTATAT CTCACTACAAACGGTGTCAATGCTGATGTCAAGT | <u>348</u> | Parainfluenza |
| PBPI_00005 | GAACAAAAACAGATGGGTTTCATTGTCAAAAACGAGAG ACATGGAGTATGAAAGAACCACAGAGTGGTTGTT | <u>349</u> | Parainfluenza |
| PBPI_00006 | TGTTCCAAGGGCAAAGAGAGAATGCGGATCTAGAGG CATTGCTTCAGACATATGGATATCCTGCATGTCT | <u>350</u> | Parainfluenza |
| PBPI_00007 | GGTATATCCCTCTTCCAGCCACATCATGACAAAAG GGGCATTTCTAGGTGGAGCAGATATCAAAGAATG | <u>351</u> | Parainfluenza |

| seqid | sequence (5'-3') | SEQ ID NO: | species |
|------------|---|------------|--------------------------|
| PBPI_00008 | GTATAACAACCACATGTACATGCAACGGTATTGGCA ATAGAATCAATCAACCACCTGATCAAGGAGTAAA | <u>352</u> | Parainfluenza |
| PBPI_00009 | CCCAACCCATTCAAACGAAAATCTCAAAAAGAGATT GGCAACACAACAAACACTGAACATCATGCCAACC | <u>353</u> | Parainfluenza |
| PBME_00001 | AAAAGTGTATCACAGAAGTTTGTTCATTGAGTATGG CAAAGCATTAGGCTCATCATCTACAGGCAGCAAA | <u>354</u> | Human metapneumovirus |
| PBME_00002 | GAAAGTCTATTTGTTAATATATTCATGCAAGCTTAT GGAGCCGGTCAAACAATGCTAAGGTGGGGGGTCA | <u>355</u> | Human metapneumovirus |
| PBME_00003 | ACGCTGTTGTGTGGAGAAATTCTGTATGCTAAACAT GCTGATTACAAATATGCTGCAGAAATAGGAATAC | <u>356</u> | Human metapneumovirus |
| PBME_00004 | TTAAGGAATCATCAGGTAATATCCCACAAAATCAGA GGCCCTCAGCACCAGACACACCCATAATCTTATT | <u>357</u> | Human metapneumovirus |
| PBME_00005 | TGAGCAATCAAAGGAGTGCAACATCAACATATCCAC TACAAATTACCCATGCAAAGTCAGCACAGGAAGA | <u>358</u> | Human metapneumovirus |
| PBME_00006 | CTGTTCCATTGGCAGCAACAGAGTAGGGATCATCAA GCAGCTGAACAAAGGTTGCTCCTATATAACCAAC | <u>359</u> | Human metapneumovirus |
| PBME_00007 | ACTTAATGACAGATGCTGAACTAGCCAGGGCCGTTT CTAACATGCCGACATCTGCAGGACAAATAAAATT | <u>360</u> | Human metapneumovirus |
| PBME_00008 | AAAAAAGGGAACTATGCTTGCCTCTTAAGAGAAG ACCAAGGTGGTATTGTGTCAGAAATGCAGGGTCAAC | <u>361</u> | Human metapneumovirus |
| PBME_00009 | GAAAAGAACACACCAGTTACAATACCAGCATTTATC AAATCGGTTTCTATCAAAGAGAGTGAATCAGCCA | <u>362</u> | Human metapneumovirus |
| PBME_00010 | CAAATCAGTTGGCAAAAAACACATGATCTGATCGC ATTATGTGATTTTATGGATCTAGAAAAGAACACA | <u>363</u> | Human metapneumovirus |
| PBME_00011 | CAGCTAAAGACACTGACTATAACTACTCTGTATGCT GCATCACAAGTGGTCCAATACTAAAAGTGAATG | <u>364</u> | Human metapneumovirus |
| PBME_00012 | AAAAGAACACACCAGTTACAATACCAGCATTTATCA AATCGGTTTCTATCAAAGAGAGTGAATCAGCCAC | <u>365</u> | Human metapneumovirus |
| PBME_00013 | CTATTATAGGAGAAAAAGTGAACACTGTATCTGAAA CATTGGAATTACCTACTATCAGTAGACCCACCAA | <u>366</u> | Human metapneumovirus |
| PBME_00014 | AAGTTAGCATGGACAGACAAAGGTGGGGCAATCAAA ACTGAAGCAAAGCAAACAATCAAAGTTATGGATC | <u>367</u> | Human metapneumovirus |
| PBME_00015 | CAGGAAAATACACAAAGTTGGAGAAAAGATGCTCTAG ACTTGCTTTCAGACAATGAAGAAGAAGATGCAGA | <u>368</u> | Human metapneumovirus |
| PBME_00016 | CTAATAGCAGACATAATAAAAGAAGCCAAGGGAAAA GCAGCAGAAATGATGGAAGAAGAAATGAACCAGC | <u>369</u> | Human metapneumovirus |

| seqid | sequence (5' - 3') | SEQ ID NO: | species |
|------------|--|------------|--------------------------|
| PBCP_00001 | ACCCTTATCGTTAGTTGCCAGCACTTAGGGTGGGAA CTCTAACGAGACTGCCTGGGTAAACCAGGAGGAA | <u>370</u> | Chlamydophila pneumoniae |
| PBCP_00002 | ATAAGAGAGGTTGGCTAATATCCAATTGATTTGAGC GTACCAGGTAAAGAAGCACCGGCTAACTCCGTGC | <u>371</u> | Chlamydophila pneumoniae |
| PBCP_00003 | CATGGGATCTTAAGTTTTAGTTGAATACTTCTGGAA AGTTGAACGATACAGGGTGATAGTCCCGTAAACG | <u>372</u> | Chlamydophila pneumoniae |
| PBCP_00004 | GGGTGCTAGCGTTAATCGGATTTATTGGGCGTAAAG GGCGTGTAGGCGGAAAGGAAAGTTAGATGTTAAA | <u>373</u> | Chlamydophila pneumoniae |
| PBCP_00005 | GCCAGGGAGTTAAGTTAAACGGCGAGATTAAGGGAT TTACATTCCGGAGTCGAAGCGAAAGCGAGTTTTA | <u>374</u> | Chlamydophila pneumoniae |
| PBCP_00006 | GCCAGGGAGTTAAGTTAAACGGCGAGATTAAGGGAT TTACATTCCGGAGTCGAAGCGAAAGCGAGTTTTA | <u>375</u> | Chlamydophila pneumoniae |

Please replace Table 16, beginning on page 38 and bridging to page 42, with a new Table 16 as follows:

Table 16. Exemplary probes for non-SARS-CoV infectious organisms damaging host's immune system

| id | sequence (5' - 3') | SEQ ID NO: | species |
|-------------|---|------------|---------|
| PBHAV_00001 | GGTGTGAACCTGAGAAAAATATTTACACCAAACCTGTGGC CTCAGATTATTGGGATGGATATAGTGGAC | <u>376</u> | HAV |
| PBHAV_00002 | ACTGAGGAGCATGAAATAATGAAGTTTTCTTGGAGAGGAGT GACTGCTGATACTAGGGCTTTGAGAAGAT | <u>377</u> | HAV |
| PBHAV_00003 | CATGGCGTGACTAAGCCCAAACAAGTGATTAAATTGGATGC AGATCCAGTAGAGTCCCAGTCAACTCTAG | <u>378</u> | HAV |
| PBHAV_00004 | GTGCAGTGATGGACATTACAGGAGTGCAGTCAACCTTGAGA TTTCGTGTTCCCTTGGATTTCTGATACACC | <u>379</u> | HAV |
| PBHAV_00005 | CCAAAAGAGATTTAATTTGGTTGGATGAAAATGGTTTGCTG TTAGGAGTTCACCCAAGATTGGCCCAGAG | <u>380</u> | HAV |
| PBHAV_00006 | AGAGATGCTTTGGATAGGGTAACAGCGGCGGATATTGGTGA GTTGTTAAGACAAAACCATTCACGCCG | <u>381</u> | HAV |
| PBHBV_00001 | GCTGGATGTGTCTGCGGCGTTTTATCATATTCCCTCTTCATC CTGCTGCTATGCCTCATCTTCTTATTGGT | <u>382</u> | HBV |
| PBHBV_00002 | ATATACATCCTTTCCATAGCTGCTAGGTTGTACTGCCAACT AGATTCTTCGCGGGACGTCCTTTGTCTAC | <u>383</u> | HBV |
| PBHBV_00003 | ATTCTTTCCCGATCATCAGTTGGACCCTGCATTCCGAGCCA ATTCAAACAATCCAGATTGGGACTTCAAC | <u>384</u> | HBV |

| id | sequence (5' - 3') | SEQ ID NO: | species |
|-------------|---|------------|---------|
| PBHBV_00004 | CTCATGTTGCTGTACAAAACCTACGGATGGAAATTGCACCT GTATTCCCATCCCATCATCTTGGGCTTTC | <u>385</u> | HBV |
| PBHBV_00005 | AGAGTCTAGACTCGTGGTGGACTTCTCTCAATTTTCTAGGG GGAGCACCCGTGTGTCTTGGCCAAAATTC | <u>386</u> | HBV |
| PBHBV_00006 | CCTTGGATGGCTTTGGGGCATGGACATTGACCCTTATAAAG AATTGGAGCTACTGTGGAGTTACTCTCA | <u>387</u> | HBV |
| PBHCV_00001 | TGGGAGACAGCAAGACACACTCCAGTCAATTCTGGCTAGG CAACATAATCATGTTTGGCCCCACACTGT | <u>388</u> | HCV |
| PBHCV_00002 | TGAGCGACTTTAAGACCTGGCTGAAAGCCAAGCTCATGCCA CAACTGCCTGGGATTCCCTTTGTGT | <u>389</u> | HCV |
| PBHCV_00003 | TATAGATGCCCACTTTCTATCCCAGACAAAGCAGAGTGGGG AGAACTTTCCTTACCTGGTAGCGTACCAA | <u>390</u> | HCV |
| PBHCV_00004 | TAACAACACCAGGCCACCGCTGGGCAATTGGTTCGGTTGTA CCTGGATGAACCAACTGGATTACCAAAA | <u>391</u> | HCV |
| PBHCV_00005 | TTTATCCCTGTGGAGAACCTAGAGACAACCATGAGATCCCC GGTGTTACGGACAACCTCTTCCACCAG | <u>392</u> | HCV |
| PBHCV_00006 | TTTATCCCTGTGGAGAACCTAGAGACAACCATGAGATCCCC GGTGTTACGGACAACCTCTTCCACCAG | <u>393</u> | HCV |
| PBHDV_00001 | TTCCCTTCTCTCGTCTTCCTCGGTCAACCTCTTAAGTTCCT CTTCTTCTTCCTTGCTGAGGTGCTTCCCT | <u>394</u> | HDV |
| PBHDV_00002 | TAAGCCCATAGCGATAGGGAGAGATGCTAGGAGTTAGAGGA GACCGAAGCGAGGAGGAAAGCAAAGAGAG | <u>395</u> | HDV |
| PBHDV_00003 | TTGGAGAGCACTCCGGCCGAAAGGTGAGGTACCCAGAAAG AGGAATCTCACGGAGAAAAGCAGACAAAT | <u>396</u> | HDV |
| PBHDV_00004 | TTAAGTTCCTCTTCTTCTTCCTTGCTGAGGTGCTTCCCTCC CGCGGCCAGCTGCTTTCTCTTGTTCTCGA | <u>397</u> | HDV |
| PBHDV_00005 | AAAAAGAGAAAGCAAGAGACGGACGATTTCCTCATGACTCT GGAGACATCCTGGAAGGGGAAAGAAGGAA | <u>398</u> | HDV |
| PBHDV_00006 | AAGTTCCTCTTCTTCTTCTTCCTTGCTGAGGTGCTTCCCTCCCG CGGCCAGCTGCTTTCTCTTGTTCTCGAGG | <u>399</u> | HDV |
| PBHGV_00001 | TCATATCATGCATCATTTGGACACGGCCCCCTTCTGCTCCAC TTGGCTTGCTGAGTGCAATGCAGAT | <u>400</u> | HGV |
| PBHGV_00002 | TAAAGTGGGAAAGTGAGTTTTGGAGATGGACTGAACAGCTG GCCTCCAACCTACTGGATTCTGGAATACCT | <u>401</u> | HGV |
| PBHGV_00003 | TAGGTCGTAAATCCCGGTCACCTTGGTAGCCACTATAGGTG GGTCTTAAGAGAAGGTTAAGATTCTCTT | <u>402</u> | HGV |

| id | sequence (5' - 3') | SEQ ID NO: | species |
|--------------|--|------------|---------|
| PBHG_V_00004 | TTCTTGGTTTGCCTCCACCAGTGGTCGCGACTCGAAGATAG ATGTGTGGAGTTTAGTGCCAGTTGG | <u>403</u> | HGV |
| PBHG_V_00005 | TCCAACACTGGAATCTGGAATACCTCTGGAAGGTCCCATT TGATTTCTGGAGAGGCGTGATAAGCCTGA | <u>404</u> | HGV |
| PBHG_V_00006 | ACGTTACCAAGGTCTTCATGTATCCCGGACAGTTACTTTCA GCAAGTTGACTATTGCGACAAGGTCTCAG | <u>405</u> | HGV |
| PBTTV_00001 | TGTCAGTAACAGGGTTCGCCATAGACTTCGGCCTCCATTTT ACCTTGTAACAACTACCAAAATGGCCGTT | <u>406</u> | TTV |
| PBTTV_00002 | ATGTCATCCATTTCTTGGGCGGGTCTACGTCTCATATAA GTAAGTGCCTTCCGAATGGCTGAGTTT | <u>407</u> | TTV |
| PBTTV_00003 | GGGATCTAGCATCCTTATTTCAAATAGCACCATAAACATGT TTGGTGACCCCAAACCTTACAACCTTCC | <u>408</u> | TTV |
| PBTTV_00004 | TGTTAGAAATCCCTGCAAAGAAACCCACTCCTCGGGCAATA GAGTCCCTAGAAGCTTACAATCGTTGAC | <u>409</u> | TTV |
| PBTTV_00005 | TCAAGGATTGACGTAAAGGTAAAGGTATCCTCGGCGGAA GCTACACAAAATGGTGGACAACATCTTCC | <u>410</u> | TTV |
| PBB19_00001 | GGCATGGTTAACTGGAATAATGAAAACCTTCCATTTAATGA TGTCAGGGGAAAAGCTTGGTGGTCTGGG | <u>411</u> | B19 |
| PBB19_00002 | GGCAAGAAAAATACACTGTGGTTTTATGGGCGCCAAAGTAC AGGAAAAACAACTTGGCAATGGCCATTG | <u>412</u> | B19 |
| PBB19_00003 | GCCATTTCTCATGGTCAGACCACTTATGGTAACGCTGAAGA CAAAGAGTATCAGCAAGGAGTGGGTAGAT | <u>413</u> | B19 |
| PBB19_00004 | AATTTTCGAGAATTTACCCAGATTTGGTGCGGTGTAGCTGC CATGTGGGAGCTTCTAATCCCTTTTCTGT | <u>414</u> | B19 |
| PBHCMV_00001 | AGGTGCGCAACGCTTTTATGAAGGTAAAGCCCGTGGCCAG GAGATTATCCGTATCTGCATACTCGCTAA | <u>415</u> | HCMV |
| PBHCMV_00002 | TAAACGACATGTATCTGTTGTTGACGCTGCGACACTTGCAG CTGCGACACGCGCTGGAGCTACAAATGAT | <u>416</u> | HCMV |
| PBHCMV_00003 | CAAAGCAGCGTCAACAACAGCCACACAGAAACCTACGTGGA GACGACACGGGACTTTTTATTGACGGAGA | <u>417</u> | HCMV |
| PBHCMV_00004 | TGCTCCAAAGCAGCGTCAACAACAGCCACACAGAAACCTAC GTGGAGACGACACGGGACTTTTTATTGAC | <u>418</u> | HCMV |
| PBEV_00001 | GAGTTAAAAGCAACTACTGTTTATTTTCCAAAATGAGCTGG GTATAGTTGATGATCTGTAGGCGCAGCTC | <u>419</u> | EBV |
| PBEV_00002 | ACAGTGACAGTGGGAGAAACACGGCCTCTGAGACATGTATG GGGGTGTTCATCTCACGCAGAAAATCTTT | <u>420</u> | EBV |

| id | sequence (5' - 3') | SEQ ID NO: | species |
|--------------|---|------------|---------|
| PBEV_00003 | TGAAGAAGTCCCGTAGTGAAAAATGGGATCTGTCTACACCA TGTCTGGTGTGCCGGGAACATATTGATCG | <u>421</u> | EBV |
| PBEV_00004 | TGAAGAAGTCCCGTAGTGAAAAATGGGATCTGTCTACACCA TGTCTGGTGTGCCGGGAACATATTGATCG | <u>422</u> | EBV |
| PBHIV1_00001 | ATTATTGTCTGGTATAGTGCAGCAGCAGAACAATTTGCTGA GGGCTATTGAGGCGCAACAGCATCTGTTG | <u>423</u> | HIV1 |
| PBHIV1_00002 | GCAACCCTCTATTGTGTGCATCAAAGGATAGAGATAAAAGA CACCAAGGAAGCTTTAGACAAGATAGAGG | <u>424</u> | HIV1 |
| PBHIV1_00003 | TGTATGTAGGATCTGACTTAGAAATAGGGCAGCATAGAACA AAATAGAGGAGCTGAGACAACATCTGTT | <u>425</u> | HIV1 |
| PBHIV1_00004 | GGAATGCTAGTTGGAGTAATAAATCTCTGGAACAGATTTGG AATCACACGACCTGGATGGAGTGGGACAG | <u>426</u> | HIV1 |
| PBTP_00001 | TACCTTGAAAGACGTTACCGCCAAAATGCTCATCAAAAGAA CGAGGACCATGCTGACAGCACCCGCGACA | <u>427</u> | TP |
| PBTP_00002 | TTTCGTGATCCTTTTTCCTTTTTCCTGTAGCTCAGCGTCCTTT TTATCTAATTCTCTGCACGCTCCCCGAG | <u>428</u> | TP |
| PBTP_00003 | TCTTTCTGACTCGCGCAAAAGGCATTACTGGAACACTATTT TAGCCATGTGGTGGCTCCCTGCTATCTTA | <u>429</u> | TP |
| PBTP_00004 | ACCTTGAAAGACGTTACCGCCAAAATGCTCATCAAAAGAAC GAGGACCATGCTGACAGCACCCGCGACAA | <u>430</u> | TP |
| PBHEV_00001 | AATAATTCACGCCGTCGCTCCTGATTATAGGTTGGAACATA ACCCAAAGATGCTTGAGGCTGCCTACCGG | <u>431</u> | HEV |
| PBHEV_00002 | TTTGTTGACGGGGCGGTTTTAGAGACTAATGGCCCAGAGCG CCACAATCTCTCTTTTGATGCCAGTCAGA | <u>432</u> | HEV |
| PBHEV_00003 | ATTTTACTAGTACTAATGGTGTGCGTGAGATCGGCCGCGGG ATAGCGCTTACCCTGTTTAACCTTGCTGA | <u>433</u> | HEV |
| PBHEV_00004 | AGTCCACTTACGGCTCTTCGACCGGCCAGTCTATGTCTCT GACTCTGTGACCTTGGTTAATGTAG | <u>434</u> | HEV |

Please replace Table 17, beginning on page 43 and bridging to page 44, with a new Table 17 as follows:

Table 17. Exemplary probes for non-SARS-CoV coronaviridae virus

| seqid | sequence (5' -3') | SEQ ID NO: |
|--------------|---|------------|
| PBIBV_00001 | GGTATAGTGTGGGTTGCTGCTAAGGGTGCTGATACTAAATCTAGATCCAAT CAGGGTACAAGAGATCCTG | <u>435</u> |
| PBIBV_00002 | GGTATAGTGTGGGTTGCTGCTAAGGGTGCTGATACTAAATCTAGATCCAAT CAGGGTACAAGAGATCCTG | <u>436</u> |
| PBMHV_00001 | CCAGCCCAAGCAAGTAACGAAGCAAAGTGCCAAAGAAGTCAGGCAGAAAAT TTTAAACAAGCCTCGCCAA | <u>437</u> |
| PBMHV_00002 | TCTAAACTTTAAGGATGTCTTTTGTTCCTGGGCAAGAAAATGCCGGTGGCA GAAGCTCCTCTGTAAACCG | <u>438</u> |
| PBEQ_00001 | AGGATCAAGAAATAGATCCAATTCCGGCACTAGAACACCCACCTCTGGTGT GACATCTGATATGGCTGAT | <u>439</u> |
| PBEQ_00002 | TTTAAACAGCCGATGGCAATCAACGCCAATTGTTGCCACGCTGGTATTTT TACTACTTGGGAACAGGCC | <u>440</u> |
| PBCA_00001 | TTGGAAC TTATGTCCGAGAGACTTTGTACCCAAAGGAATAGGTAACAAGGA TCAACAGATTGGTTATTGG | <u>441</u> |
| PBCA_00002 | GCTGAATGTGTTCCATCTGTATCTAGCATTCTGTTTGGAAGCTATTGGACT GCAAAGGAAGATGGCGACC | <u>442</u> |
| PBFE_00001 | CACCACCCTCGAACAAGGAGCTAAATTTTGGTATGTATGTCCGAGAGACTT TGTTCCTCAAGGGAATAGGT | <u>443</u> |
| PBFE_00002 | GGCACTCGTGGAACCAACAATGAATCCGAACCATTTGAGATTTGATGGTAAG ATACCACCACAATTCCAGC | <u>444</u> |
| PBPEDV_00001 | CTGATCCAAATGTTGAGCTTCTTGTGTCACAGGTGGATGCATTTAAACTG GGAATGCAAAACCCAGAG | <u>445</u> |
| PBPEDV_00002 | ATGAGCAAATTCGCTGGCGTATGCGCCGTGGTGAGCGAATTGAACAACCTT CAAATTGGCATTTC TACTA | <u>446</u> |
| PBPTGV_00001 | GAGAGACTTTGTACCCAAAGGAATAGGTAACAGGGATCAACAGATTGGTTA TTGGAATAGACAAACTCGC | <u>447</u> |
| PBPTGV_00002 | GATGGTGACCAGATAGAAGTCACGTTACACACAAAATACCACTTGCCAAAG GATGATCCTAAACTGGAC | <u>448</u> |
| PBBOV_00001 | TATTTT TACTATCTTGGAACAGGACCGCATGCCAAAGACCAGTATGGCACC GACATTGACGGAGTCTACT | <u>449</u> |
| PBBOV_00002 | AGAACCCCTACCTCTGGTGTAACACCTGATATGGCTGATCAAATTGCTAGT CTTGTCTGGCTAAACTTG | <u>450</u> |
| PBFIPV_00001 | GAGTGTGGTTAATCAACAGGGTGAAGCGCTGAGTCAACTTACCAGTCAGTT ACAGAAAACTTCCAGGCT | <u>451</u> |
| PBFIPV_00002 | CCGGCATTGTAGATGGTAATAAGATGGCCATGTACACAGCATCTTTAATTG GAGGTATGGCTTTGGGCTC | <u>452</u> |

| seqid | sequence (5' - 3') | SEQ ID NO: |
|--------------|--|------------|
| PBR_00001 | AAATGTTAAAACTTGGAACTAGTGATCCACAGTTCCCCATTCTTGCAGAGT TGGCCCCAACACCTGGTGC | <u>453</u> |
| PBR_00002 | CCCATTA CTCTTGGTTTTCGGGCATTACCCAATTTCAAAGGGAAAGGAGT TCCAGTTTGCAGATGGGCA | <u>454</u> |
| PBPHEV_00001 | TAGTAACCAGGCTGATATTAATACCCCGGCTGACATTGTGATCGGGATCC AAGTAGCGATGAGGCTATT | <u>455</u> |
| PBPHEV_00002 | TTCTTTTAAACAGCCGATGGCAATCAGCGTCAACTGCTGCCACGATGGTA CTTTTACTACCTGGGAACA | <u>456</u> |
| PBPV_00001 | GTGGTTCCCCATTACTCCTGGTTTCTGGCATTACCCAATTCCAGAAGGGA AAGGAGTTTAAGTTTGCAG | <u>457</u> |
| PBPV_00002 | AAGAAGTCAGGCAGAAAATTTTAAACAAGCCTCGCCAAAAGAGGACTCCAA ACAAGCAGTGCCCAAGTCA | <u>458</u> |
| PBTK_00001 | TTTGGTGATGACAAGATGAATGAGGAAGGTATTAAGGATGGGCGTGTTACG GCAATGCTCAACCTAGTCC | <u>459</u> |
| PBTK_00002 | TTTGGTGATGACAAGATGAATGAGGAAGGTATTAAGGATGGGCGTGTTACG GCAATGCTCAACCTAGTCC | <u>460</u> |
| PBSDAV_00001 | AGCCTGCCTCTACTGTAAAACCTGATATGGCCGAAGAAATTGCTGCTCTTG TTTTGGCTAAGCTAGGCAA | <u>461</u> |
| PBSDAV_00002 | CCCCATTCTTGCAGAGTTGGCCCCAACACCTGGTGCCTTCTTCTTTGGATC TAAATTAGAATTGGTCAAA | <u>462</u> |

Please replace Table 18, beginning on page 50 and bridging to page 54, with a new Table 18 as follows:

Table 18. Exemplary SARS-CoV primers

| id | sequence (5' - 3') | SEQ ID NO: | region |
|------------|---|------------|-------------------------------|
| PMSL_00005 | CACGTCTCCCAAATGCTTGAGTGACG | <u>463</u> | SARS-Cov Nucleocapsid gene |
| PMSU_00006 | CCTCGAGGCCAGGGCGTTCC | <u>464</u> | SARS-Cov Nucleocapsid gene |
| PMV_00039 | TCACTTGCTTCCGTTGAGGTCGGGGACCAAGACC TAATCAGA | <u>465</u> | SARS-Cov Nucleocapsid gene |
| PMV_00040 | GGTTTCGGATGTTACAGCGTAGCCGCAGGAAGAA GAGTCACAG | <u>466</u> | SARS-Cov Nucleocapsid gene |
| PMV_00041 | TCACTTGCTTCCGTTGAGGAGGCCAGGGCGTTCC AATC | <u>467</u> | SARS-Cov Nucleocapsid gene |

| id | sequence(5'-3') | SEQ ID NO: | region |
|------------|---|------------|-------------------------------|
| PMV_00042 | GGTTTCGGATGTTACAGCGTCAATAGCGCGAGGG CAGTTTC | <u>468</u> | SARS-Cov Nucleocapsid gene |
| PMV_00043 | TCACTTGCTTCCGTTGAGGGGCACCCGCAATCCT AATAACAA | <u>469</u> | SARS-Cov Nucleocapsid gene |
| PMV_00044 | GGTTTCGGATGTTACAGCGTAGCCGCAGGAAGAA GAGTCACAG | <u>470</u> | SARS-Cov Nucleocapsid gene |
| PMV_00090 | TCGGGGACCAAGACCTAATCAGA | <u>471</u> | SARS-Cov Nucleocapsid gene |
| PMV_00091 | AGCCGCAGGAAGAAGAGTCACAG | <u>472</u> | SARS-Cov Nucleocapsid gene |
| PMV_00092 | AGGCCAGGGCGTTCCAATC | <u>473</u> | SARS-Cov Nucleocapsid gene |
| PMV_00093 | CAATAGCGCGAGGGCAGTTTC | <u>474</u> | SARS-Cov Nucleocapsid gene |
| PMV_00094 | GGCACCCGCAATCCTAATAACAA | <u>475</u> | SARS-Cov Nucleocapsid gene |
| PMV_00095 | AGCCGCAGGAAGAAGAGTCACAG | <u>476</u> | SARS-Cov Nucleocapsid gene |
| PMSL_00001 | ACATCACAGCTTCTACACCCGTTAAGGT | <u>477</u> | SARS-Cov Replicase 1A |
| PMSL_00002 | ATACAGAATACATAGATTGCTGTTATCC | <u>478</u> | SARS-Cov Replicase 1A |
| PMSU_00002 | GCATCGTTGACTATGGTGTCCGATTCT | <u>479</u> | SARS-Cov Replicase 1A |
| PMSU_00003 | GCTGCATTGGTTTGTATATCGTTATGC | <u>480</u> | SARS-Cov Replicase 1A |
| PMV_00023 | TCACTTGCTTCCGTTGAGGAGCCGCTTGTCACAA TGCCAATT | <u>481</u> | SARS-Cov Replicase 1A |
| PMV_00024 | GGTTTCGGATGTTACAGCGTCATCACCAAGCTCG CCAACAGTT | <u>482</u> | SARS-Cov Replicase 1A |
| PMV_00025 | TCACTTGCTTCCGTTGAGGAGGTTGCCATCATTT TGGCATCTT | <u>483</u> | SARS-Cov Replicase 1A |
| PMV_00026 | GGTTTCGGATGTTACAGCGTCTTTGCGCCAGCGA TAGTGACTT | <u>484</u> | SARS-Cov Replicase 1A |
| PMV_00027 | TCACTTGCTTCCGTTGAGGATGGCACCCGTTTCT GCAATGG | <u>485</u> | SARS-Cov Replicase 1A |

| id | sequence(5'-3') | SEQ ID NO: | region |
|-----------|--|------------|--------------------------|
| PMV_00028 | GGTTTCGGATGTTACAGCGTTCGGGCAGCTGACA CGAATGTAGA | <u>486</u> | SARS-Cov Replicase 1A |
| PMV_00029 | TCACTTGCTTCCGTTGAGGGAATGGCGATGTAGT GGCTATTGA | <u>487</u> | SARS-Cov Replicase 1A |
| PMV_00030 | GGTTTCGGATGTTACAGCGTTAATGCCGGCATCC AAACATAAT | <u>488</u> | SARS-Cov Replicase 1A |
| PMV_00031 | TCACTTGCTTCCGTTGAGGTAGCCAGCGTGGTGG TTCATACAA | <u>489</u> | SARS-Cov Replicase 1A |
| PMV_00032 | GGTTTCGGATGTTACAGCGTCTCCCGGCAGAAAG CTGTAAGCT | <u>490</u> | SARS-Cov Replicase 1A |
| PMV_00033 | TCACTTGCTTCCGTTGAGGTATAGAGCCCGTGCT GGTGATGC | <u>491</u> | SARS-Cov Replicase 1A |
| PMV_00034 | GGTTTCGGATGTTACAGCGTATCGCCATTCAAGT CTGGGAAGAA | <u>492</u> | SARS-Cov Replicase 1A |
| PMV_00035 | TCACTTGCTTCCGTTGAGGTGGCTCAGGCCATAC TGGCATTAC | <u>493</u> | SARS-Cov Replicase 1A |
| PMV_00036 | GGTTTCGGATGTTACAGCGTTTTGCGCCAGCGAT AGTGACTTG | <u>494</u> | SARS-Cov Replicase 1A |
| PMV_00037 | TCACTTGCTTCCGTTGAGGTTCCTCGTCAGGCAAA GTTGAAGG | <u>495</u> | SARS-Cov Replicase 1A |
| PMV_00038 | GGTTTCGGATGTTACAGCGTGACGGCAATTCCTG TTTGAGCAGA | <u>496</u> | SARS-Cov Replicase 1A |
| PMV_00074 | AGCCGCTTGTCACAATGCCAATT | <u>497</u> | SARS-Cov Replicase 1A |
| PMV_00075 | CATCACCAAGCTCGCCAACAGTT | <u>498</u> | SARS-Cov Replicase 1A |
| PMV_00076 | AGGTTGCCATCATTTTGGCATCTT | <u>499</u> | SARS-Cov Replicase 1A |
| PMV_00077 | CTTTGCGCCAGCGATAGTGACTT | <u>500</u> | SARS-Cov Replicase 1A |
| PMV_00078 | ATGGCACCCGTTTCTGCAATGG | <u>501</u> | SARS-Cov Replicase 1A |
| PMV_00079 | TCGGGCAGCTGACACGAATGTAGA | <u>502</u> | SARS-Cov Replicase 1A |
| PMV_00080 | GAATGGCGATGTAGTGGCTATTGA | <u>503</u> | SARS-Cov Replicase 1A |

| id | sequence (5'-3') | SEQ ID NO: | region |
|-----------|---|------------|--------------------------|
| PMV_00081 | TAATGCCGGCATCCAAACATAAT | <u>504</u> | SARS-Cov Replicase 1A |
| PMV_00082 | TAGCCAGCGTGGTGGTTCATACAA | <u>505</u> | SARS-Cov Replicase 1A |
| PMV_00083 | CTCCCGGCAGAAAGCTGTAAGCT | <u>506</u> | SARS-Cov Replicase 1A |
| PMV_00084 | TATAGAGCCCGTGCTGGTGATGC | <u>507</u> | SARS-Cov Replicase 1A |
| PMV_00085 | ATCGCCATTCAAGTCTGGGAAGAA | <u>508</u> | SARS-Cov Replicase 1A |
| PMV_00086 | TGGCTCAGGCCATACTGGCATTAC | <u>509</u> | SARS-Cov Replicase 1A |
| PMV_00087 | TTTGCGCCAGCGATAGTGACTTG | <u>510</u> | SARS-Cov Replicase 1A |
| PMV_00088 | TTCCCGTCAGGCAAAGTTGAAGG | <u>511</u> | SARS-Cov Replicase 1A |
| PMV_00089 | GACGGCAATTCTCTGTTTGAGCAGA | <u>512</u> | SARS-Cov Replicase 1A |
| PMV_00003 | TCACTTGCTTCCGTTGAGGATGAATTACCAAGTC AATGGTTAC | <u>513</u> | SARS-Cov Replicase 1B |
| PMV_00004 | GGTTTCGGATGTTACAGCGTATAACCAGTCGGTA CAGCTAC | <u>514</u> | SARS-Cov Replicase 1B |
| PMV_00005 | TCACTTGCTTCCGTTGAGGGAAGCTATTTCGTCAC GTTTCG | <u>515</u> | SARS-Cov Replicase 1B |
| PMV_00006 | GGTTTCGGATGTTACAGCGTCTGTAGAAAATCCT AGCTGGAG | <u>516</u> | SARS-Cov Replicase 1B |
| PMV_00007 | TCACTTGCTTCCGTTGAGGCCTCTCTTGTTCTTG CTCGCA | <u>517</u> | SARS-Cov Replicase 1B |
| PMV_00008 | GGTTTCGGATGTTACAGCGTGTGAGCCGCCACAC ATG | <u>518</u> | SARS-Cov Replicase 1B |
| PMV_00009 | TCACTTGCTTCCGTTGAGGCTAACATGCTTAGGA TAATGG | <u>519</u> | SARS-Cov Replicase 1B |
| PMV_00010 | GGTTTCGGATGTTACAGCGTCAGGTAAGCGTAAA ACTCATC | <u>520</u> | SARS-Cov Replicase 1B |
| PMV_00011 | TCACTTGCTTCCGTTGAGGGCCTCTCTTGTTCTT GCTCGC | <u>521</u> | SARS-Cov Replicase 1B |

| id | sequence (5'-3') | SEQ ID NO: | region |
|-----------|--|------------|--------------------------|
| PMV_00013 | TCACTTGCTTCCGTTGAGGCACCGTTTCTACAGG TTAGCTAACGA | <u>522</u> | SARS-Cov Replicase 1B |
| PMV_00014 | GGTTTCGGATGTTACAGCGTAAATGTTTACGCAG GTAAGCGTAAAA | <u>523</u> | SARS-Cov Replicase 1B |
| PMV_00015 | TCACTTGCTTCCGTTGAGGTACACACCTCAGCGT TG | <u>524</u> | SARS-Cov Replicase 1B |
| PMV_00016 | GGTTTCGGATGTTACAGCGTCACGAACGTGACGA AT | <u>525</u> | SARS-Cov Replicase 1B |
| PMV_00017 | TCACTTGCTTCCGTTGAGGGCTTAGGATAATGGC CTCTC | <u>526</u> | SARS-Cov Replicase 1B |
| PMV_00018 | GGTTTCGGATGTTACAGCGTCCACGAATTCATGA TCAACATCCC | <u>527</u> | SARS-Cov Replicase 1B |
| PMV_00019 | TCACTTGCTTCCGTTGAGGGCTCGCAAACATAAC ACTTGC | <u>528</u> | SARS-Cov Replicase 1B |
| PMV_00020 | GGTTTCGGATGTTACAGCGTGAGACACTCATAGA GCCTGTG | <u>529</u> | SARS-Cov Replicase 1B |
| PMV_00055 | ATGAATTACCAAGTCAATGGTTAC | <u>530</u> | SARS-Cov Replicase 1B |
| PMV_00056 | ATAACCAGTCGGTACAGCTAC | <u>531</u> | SARS-Cov Replicase 1B |
| PMV_00057 | GAAGCTATTCGTCACGTTTCG | <u>532</u> | SARS-Cov Replicase 1B |
| PMV_00058 | CTGTAGAAAAATCCTAGCTGGAG | <u>533</u> | SARS-Cov Replicase 1B |
| PMV_00059 | CCTCTCTTGTCTTGCTCGCA | <u>534</u> | SARS-Cov Replicase 1B |
| PMV_00060 | GTGAGCCGCCACACATG | <u>535</u> | SARS-Cov Replicase 1B |
| PMV_00061 | CTAACATGCTTAGGATAATGG | <u>536</u> | SARS-Cov Replicase 1B |
| PMV_00062 | CAGGTAAGCGTAAAACTCATC | <u>537</u> | SARS-Cov Replicase 1B |
| PMV_00063 | GCCTCTCTTGTCTTGCTCGC | <u>538</u> | SARS-Cov Replicase 1B |
| PMV_00064 | CACCGTTTCTACAGGTTAGCTAACGA | <u>539</u> | SARS-Cov Replicase 1B |

| id | sequence(5'-3') | SEQ ID NO: | region |
|------------|--|------------|----------------------------------|
| PMV_00065 | AAATGTTTACGCAGGTAAGCGTAAAA | <u>540</u> | SARS-Cov Replicase 1B |
| PMV_00066 | TACACACCTCAGCGTTG | <u>541</u> | SARS-Cov Replicase 1B |
| PMV_00067 | CACGAACGTGACGAAT | <u>542</u> | SARS-Cov Replicase 1B |
| PMV_00068 | GCTTAGGATAATGGCCTCTC | <u>543</u> | SARS-Cov Replicase 1B |
| PMV_00069 | CCACGAATTCATGATCAACATCCC | <u>544</u> | SARS-Cov Replicase 1B |
| PMV_00070 | GCTCGCAAACATAACACTTGC | <u>545</u> | SARS-Cov Replicase 1B |
| PMV_00071 | GAGACACTCATAGAGCCTGTG | <u>546</u> | SARS-Cov Replicase 1B |
| PMSL_00003 | CCAGCTCCAATAGGAATGTCGCACTC | <u>547</u> | SARS-Cov Spike glycoprotein gene |
| PMSL_00004 | TCCGCAGATGTACATATTACAATCTACG | <u>548</u> | SARS-Cov Spike glycoprotein gene |
| PMSU_00005 | TTAAATGCACCGGCCACGGTTTG | <u>549</u> | SARS-Cov Spike glycoprotein gene |
| PMV_000100 | ATAGCGCCAGGACAACTGGTGTT | <u>550</u> | SARS-Cov Spike glycoprotein gene |
| PMV_000101 | TATATGCGCCAAGCTGGTGTGAGT | <u>551</u> | SARS-Cov Spike glycoprotein gene |
| PMV_000102 | CGAGGCGGAGGTACAAATTGACAG | <u>552</u> | SARS-Cov Spike glycoprotein gene |
| PMV_000103 | ATGAAGCCGAGCCAAACATACCAA | <u>553</u> | SARS-Cov Spike glycoprotein gene |
| PMV_00045 | TCACTTGCTTCCGTTGAGGATGCACCGGCCACGG TTTGTG | <u>554</u> | SARS-Cov Spike glycoprotein gene |
| PMV_00046 | GGTTTCGGATGTTACAGCGTATGCGCCAAGCTGG TGTGAGTTGA | <u>555</u> | SARS-Cov Spike glycoprotein gene |
| PMV_00047 | TCACTTGCTTCCGTTGAGGTGCTGGCGCTGCTCT TCAAATACC | <u>556</u> | SARS-Cov Spike glycoprotein gene |
| PMV_00048 | GGTTTCGGATGTTACAGCGTCGGGGCTGCTTGTG GGAAGG | <u>557</u> | SARS-Cov Spike glycoprotein gene |

| id | sequence (5'-3') | SEQ ID NO: | region |
|-----------|--|------------|-------------------------------------|
| PMV_00049 | TCACTTGCTTCCGTTGAGGATAGCGCCAGGACAA ACTGGTGTT | <u>558</u> | SARS-Cov Spike glycoprotein gene |
| PMV_00050 | GGTTTCGGATGTTACAGCGTTATATGCGCCAAGC TGGTGTGAGT | <u>559</u> | SARS-Cov Spike glycoprotein gene |
| PMV_00051 | TCACTTGCTTCCGTTGAGGCGAGGCGGAGGTACA AATTGACAG | <u>560</u> | SARS-Cov Spike glycoprotein gene |
| PMV_00052 | GGTTTCGGATGTTACAGCGTATGAAGCCGAGCCA AACATACCAA | <u>561</u> | SARS-Cov Spike glycoprotein gene |
| PMV_00096 | ATGCACCGGCCACGGTTTGTG | <u>562</u> | SARS-Cov Spike glycoprotein gene |
| PMV_00097 | ATGCGCCAAGCTGGTGTGAGTTGA | <u>563</u> | SARS-Cov Spike glycoprotein gene |
| PMV_00098 | TGCTGGCGCTGCTCTTCAAATACC | <u>564</u> | SARS-Cov Spike glycoprotein gene |
| PMV_00099 | CGGGGCTGCTTGTGGGAAGG | <u>565</u> | SARS-Cov Spike glycoprotein gene |

Please replace Table 19, beginning on page 54 and bridging to page 61, with a new Table 19 as follows:

Table 19. Exemplary primers for non-SARS-CoV infectious organism causing SARS-like symptoms

| id | Sequence (5' - 3') | SEQ ID NO: | species |
|------------|--------------------------|------------|-------------------|
| PMIA_00001 | TTTGTGCGACAATGCTTCA | <u>566</u> | Influenza A virus |
| PMIA_00002 | GACATTTGAGAAAGCTTGCC | <u>567</u> | Influenza A virus |
| PMIA_00003 | AGGGACAACCTNGAACCTGG | <u>568</u> | Influenza A virus |
| PMIA_00004 | AGGAGTTGAACCAAGACGCATT | <u>569</u> | Influenza A virus |
| PMIA_00005 | ACCACATTCCCTTATACTGGAG | <u>570</u> | Influenza A virus |
| PMIA_00006 | TTAGTCATCATCTTTCTCACAACA | <u>571</u> | Influenza A virus |
| PMIA_00007 | ACAAATTGCTTCAAATGAGAAC | <u>572</u> | Influenza A virus |
| PMIA_00008 | TGTCTCCGAAGAAATAAGATCC | <u>573</u> | Influenza A virus |
| PMIA_00009 | GCGCAGAGACTTGAAGATGT | <u>574</u> | Influenza A virus |
| PMIA_00010 | CCTTCCGTAGAAGGCCCT | <u>575</u> | Influenza A virus |

| id | Sequence (5' - 3') | SEQ ID NO: | species |
|-------------|---------------------------|------------|-------------------|
| PMIB_00001 | CACAATGGCAGAATTTAGTGA | <u>576</u> | Influenza B virus |
| PMIB_00002 | GTCAGTTTGATCCCGTAGTG | <u>577</u> | Influenza B virus |
| PMIB_00003 | CAGATCCCAGAGTGGACTCA | <u>578</u> | Influenza B virus |
| PMIB_00004 | TGTATTACCCAAGGGTTGTTAC | <u>579</u> | Influenza B virus |
| PMIB_00005 | GATCAGCATGACAGTAACAGGA | <u>580</u> | Influenza B virus |
| PMIB_00006 | ATGTTCGGTAAAAGTCGTTTAT | <u>581</u> | Influenza B virus |
| PMIB_00007 | CCACAGGGGAGATTCCAAAG | <u>582</u> | Influenza B virus |
| PMIB_00008 | GACATTCTTCCTGATTGATAATC | <u>583</u> | Influenza B virus |
| PMIB_00009 | CAAACAACGGTAGACCAATATA | <u>584</u> | Influenza B virus |
| PMIB_00010 | AGGTTTCAGTATCTATCACAGTCTT | <u>585</u> | Influenza B virus |
| PMIB_00011 | ATGTCCAACATGGATATTGAC | <u>586</u> | Influenza B virus |
| PMIB_00012 | GCTCTTCCTATAAATCGAATG | <u>587</u> | Influenza B virus |
| PMIB_00013 | TGATCAAGTGATCGGAAGTAG | <u>588</u> | Influenza B virus |
| PMIB_00014 | GATGGTCTGCTTAATTGGAA | <u>589</u> | Influenza B virus |
| PMIB_00015 | ACAGAAGATGGAGAAGGCAA | <u>590</u> | Influenza B virus |
| PMIB_00016 | ATTGTTTCTTTGGCCTGGAT | <u>591</u> | Influenza B virus |
| PMAd1_00001 | TGGCGGTATAGGGGTAAGT | <u>592</u> | Human adenovirus |
| PMAd1_00002 | ATTGCGGTGATGGTTAAAGG | <u>593</u> | Human adenovirus |
| PMAd1_00003 | TTTGCCGATCCCACTTATC | <u>594</u> | Human adenovirus |
| PMAd1_00004 | GCAAGTCTACCACGGCATT | <u>595</u> | Human adenovirus |
| PMAd2_00001 | CTCCGTTATCGCTCCATGTT | <u>596</u> | Human adenovirus |
| PMAd2_00002 | AAGGACTGGTCGTTGGTGTC | <u>597</u> | Human adenovirus |
| PMAd2_00003 | AAATGCCGTGGTAGATTTGC | <u>598</u> | Human adenovirus |
| PMAd2_00004 | GTTGAAGGGGTTGACGTTGT | <u>599</u> | Human adenovirus |
| PMAd3_00001 | TCCTCTGGATGGCATAGGAC | <u>600</u> | Human adenovirus |
| PMAd3_00002 | TGTTGGTGTTAGTGGGCAAA | <u>601</u> | Human adenovirus |

| id | Sequence (5' - 3') | SEQ ID NO: | species |
|--------------|----------------------|------------|------------------|
| PMAd3_00003 | ACATGGTCCTGCAAAGTTCC | 602 | Human adenovirus |
| PMAd3_00004 | GCATTGTGCCACGTTGTATC | 603 | Human adenovirus |
| PMAd4_00001 | CGCTTCGGAGTACCTCAGTC | 604 | Human adenovirus |
| PMAd4_00002 | CTGCATCATTGGTGTCAACC | 605 | Human adenovirus |
| PMAd4_00003 | GGCACCTTTTACCTCAACCA | 606 | Human adenovirus |
| PMAd4_00004 | TCTGGACCAAGAACCAGTCC | 607 | Human adenovirus |
| PMAd5_00001 | GGCCTACCCTGCTAACTTCC | 608 | Human adenovirus |
| PMAd5_00002 | ATAAAGAAGGGTGGGCTCGT | 609 | Human adenovirus |
| PMAd5_00003 | ATCGCAGTTGAATGCTGTTG | 610 | Human adenovirus |
| PMAd5_00004 | GTTGAAGGGGTGACGTTGT | 611 | Human adenovirus |
| PMAd7_00001 | ACATGGTCCTGCAAAGTTCC | 612 | Human adenovirus |
| PMAd7_00002 | GATCGAACCCTGATCCAAGA | 613 | Human adenovirus |
| PMAd7_00003 | AACACCAACCGAAGGAGATG | 614 | Human adenovirus |
| PMAd7_00004 | CCTATGCCATCCAGAGGAAA | 615 | Human adenovirus |
| PMAd11_00001 | CAGATGCTCGCCAACTACAA | 616 | Human adenovirus |
| PMAd11_00002 | AGCCATGTAACCCACAAAGC | 617 | Human adenovirus |
| PMAd11_00003 | ACGGACGTTATGTGCCTTTC | 618 | Human adenovirus |
| PMAd11_00004 | GGGAATATTGGTTGCATTGG | 619 | Human adenovirus |
| PMAd21_00001 | ACTGGTTCCTGGTCCAGATG | 620 | Human adenovirus |
| PMAd21_00002 | AGCCATGTAACCCACAAAGC | 621 | Human adenovirus |
| PMAd21_00003 | CTGGATATGGCCAGCACTTT | 622 | Human adenovirus |
| PMAd21_00004 | CACCTGAGGTTCTGGTTGGT | 623 | Human adenovirus |
| PMAd23_00001 | TAATGAAAAGGGCGGACAAG | 624 | Human adenovirus |
| PMAd23_00002 | GCCAATGTAGTTTGGCCTGT | 625 | Human adenovirus |
| PMAd23_00003 | AACTCCGCGGTAGACAGCTA | 626 | Human adenovirus |
| PMAd23_00004 | CGTAGGTGTTGGTGTGGTG | 627 | Human adenovirus |

| id | Sequence (5' - 3') | SEQ ID NO: | species |
|------------|---|------------|-------------------------------|
| PMV_a0061 | TCACTTGCTTCCGTTGAGGTTGGGGTGATGG GTTTCAGATTAA | <u>628</u> | HCoV-OC43 |
| PMV_a0062 | GGTTTCGGATGTTACAGCGTCTCGGGAAGAT CGCCTTCTTCTA | <u>629</u> | HCoV-OC43 |
| PMV_b0061 | TTGGGGTGATGGGTTTCAGATTAA | <u>630</u> | HCoV-OC43 |
| PMV_b0062 | CTCGGGAAGATCGCCTTCTTCTA | <u>631</u> | HCoV-OC43 |
| PMV_a0053 | TCACTTGCTTCCGTTGAGGTTGGGCTGGCGG TTTAGAGTTGA | <u>632</u> | HCoV-229E |
| PMV_a0054 | GGTTTCGGATGTTACAGCGTGTGCGACCGCC CTTGTTTATGG | <u>633</u> | HCoV-229E |
| PMV_a0055 | TCACTTGCTTCCGTTGAGGGCGTTGTTGGCC TTTTTCTTGTCT | <u>634</u> | HCoV-229E |
| PMV_a0056 | GGTTTCGGATGTTACAGCGTGCCCGGCATTA TTTCATTGTTCTG | <u>635</u> | HCoV-229E |
| PMV_a0057 | TCACTTGCTTCCGTTGAGGACAAAAGCCGCT GGTGGTAAAG | <u>636</u> | HCoV-229E |
| PMV_a0058 | GGTTTCGGATGTTACAGCGTCAGAAATCATA ACGGGCAAACCTCA | <u>637</u> | HCoV-229E |
| PMV_a0059 | TCACTTGCTTCCGTTGAGGAAGAGTTATTGC TGGCGTTGTTGG | <u>638</u> | HCoV-229E |
| PMV_a0060 | GGTTTCGGATGTTACAGCGTGCCCGGCATTA TTTCATTGTTCTG | <u>639</u> | HCoV-229E |
| PMV_b0053 | TTGGGCTGGCGGTTTAGAGTTGA | <u>640</u> | HCoV-229E |
| PMV_b0054 | GTGCGACCGCCCTTGTATTATGG | <u>641</u> | HCoV-229E |
| PMV_b0055 | GCGTTGTTGGCCTTTTCTTGTCT | <u>642</u> | HCoV-229E |
| PMV_b0056 | GCCCCGCATTATTTTCATTGTTCTG | <u>643</u> | HCoV-229E |
| PMV_b0057 | ACAAAAGCCGCTGGTGGTAAAG | <u>644</u> | HCoV-229E |
| PMV_b0058 | CAGAAATCATAACGGGCAAACCTCA | <u>645</u> | HCoV-229E |
| PMV_b0059 | AAGAGTTATTGCTGGCGTTGTTGG | <u>646</u> | HCoV-229E |
| PMV_b0060 | GCCCCGCATTATTTTCATTGTTCTG | <u>647</u> | HCoV-229E |
| PMHE_00001 | GGTGGTAACCCCTCGCAGGA | <u>648</u> | Human enteric coronaviruse |

| id | Sequence (5' - 3') | SEQ ID NO: | species |
|------------|------------------------------|------------|---------------------------|
| PMHE_00002 | TGGCTCTTCCCTTTGGGCACT | <u>649</u> | Human enteric coronavirus |
| PMHE_00003 | GAGAATGAACCTTATGTCGGCACCTG | <u>650</u> | Human enteric coronavirus |
| PMHE_00004 | TTCCGCAAGTCTTCACTTTCTCCAA | <u>651</u> | Human enteric coronavirus |
| PMHE_00005 | CAGCTTTCAGCCAGGGACGTGT | <u>652</u> | Human enteric coronavirus |
| PMHE_00006 | TTTCCAGCTTTTGCGCAGTGGT | <u>653</u> | Human enteric coronavirus |
| PMHE_00007 | TCTGTTTTGGTGCAGGTCAATTTGTG | <u>654</u> | Human enteric coronavirus |
| PMHE_00008 | ATGAACCAGGTCGTAAGCATCCTCAA | <u>655</u> | Human enteric coronavirus |
| PMHE_00009 | GTTGCTTGTC AACCCCCG TACTGTTA | <u>656</u> | Human enteric coronavirus |
| PMHE_00010 | AGGACACCTGCCATAGGGGTAGAGAG | <u>657</u> | Human enteric coronavirus |
| PMHE_00011 | GGTTGTTGACTCGCGGTGGA | <u>658</u> | Human enteric coronavirus |
| PMHE_00012 | GGGGTAGAGAGGCCAAACACTGC | <u>659</u> | Human enteric coronavirus |
| PMRh_00001 | ACATGGTCCCATTGGATTGT | <u>660</u> | Human rhinovirus |
| PMRh_00002 | TGAGGAAATCTTTCGCCACT | <u>661</u> | Human rhinovirus |
| PMRh_00003 | ATGTTGCCCCCTAGTCTGTG | <u>662</u> | Human rhinovirus |
| PMRh_00004 | TTCTGAAGGTGGTGTGTTGC | <u>663</u> | Human rhinovirus |
| PMRh_00005 | TGGTATTCATGTTGGCGGTA | <u>664</u> | Human rhinovirus |
| PMRh_00006 | ACAGCAGGTTCTTGTCACC | <u>665</u> | Human rhinovirus |
| PMRh_00007 | TCTTGCCTCCAATGGCTAGT | <u>666</u> | Human rhinovirus |
| PMRh_00008 | TGACATGCCTGCATTGAGTT | <u>667</u> | Human rhinovirus |
| PMRh_00009 | TCCCAATATGCCCTCTTCAG | <u>668</u> | Human rhinovirus |
| PMRh_00010 | CGCTGATGGGGATTGAGTAT | <u>669</u> | Human rhinovirus |

| id | Sequence (5' - 3') | SEQ ID NO: | species |
|------------|----------------------------|------------|-----------------------|
| PMRh_00011 | TGTGCTCAGTGTGCTTCCTC | <u>670</u> | Human rhinovirus |
| PMRh_00012 | TGCACCCATGATGACAATCT | <u>671</u> | Human rhinovirus |
| PMRh_00013 | GCAGTTCTTGCCAAAGAAGG | <u>672</u> | Human rhinovirus |
| PMRh_00014 | TGAAGGGTTTTTGGTCCATC | <u>673</u> | Human rhinovirus |
| PMRh_00015 | TGCCTGATGCCCTTAAAAAC | <u>674</u> | Human rhinovirus |
| PMRh_00016 | GGGTGTGATTGTACCCGACT | <u>675</u> | Human rhinovirus |
| PMMP_00001 | CTTAACAGTTGTATGCATTGGAAACT | <u>676</u> | Mycoplasma pneumoniae |
| PMMP_00002 | GTTTACGGTGTGGACTACTAGGGTAT | <u>677</u> | Mycoplasma pneumoniae |
| PMMP_00003 | CTATGCTGAGAAGTAGAATAGCCACA | <u>678</u> | Mycoplasma pneumoniae |
| PMMP_00004 | TGGTACAGTCAAACCTAGCCATTAC | <u>679</u> | Mycoplasma pneumoniae |
| PMMP_00005 | ATACCCTAGTAGTCCACACCGTAAAC | <u>680</u> | Mycoplasma pneumoniae |
| PMMP_00006 | ATGTCAAGTCTAGGTAAGGTTTTTCG | <u>681</u> | Mycoplasma pneumoniae |
| PMMP_00007 | AGGCGAAAACCTTAGGCCATT | <u>682</u> | Mycoplasma pneumoniae |
| PMMP_00008 | CCGTCAATTCGTTTGAGTT | <u>683</u> | Mycoplasma pneumoniae |
| PMMP_00009 | CGACGGTACACGAAAAACCT | <u>684</u> | Mycoplasma pneumoniae |
| PMMP_00010 | TCCCTTCCTTCCTCCAATTT | <u>685</u> | Mycoplasma pneumoniae |
| PMR_00001 | ATTCCCATGGAGAACTCCTAGAT | <u>686</u> | Rubella virus |
| PMR_00002 | GTGATCACTGACCTGCATCTG | <u>687</u> | Rubella virus |
| PMR_00003 | GTAAGAGACCACGTCCGATCAAT | <u>688</u> | Rubella virus |
| PMR_00004 | GAGGACGTGTAGGGCTTCTTTAG | <u>689</u> | Rubella virus |
| PMR_00005 | ATCGGACCTCGCTTAGGACT | <u>690</u> | Rubella virus |
| PMR_00006 | CTGGGTATCACGGCTACGAT | <u>691</u> | Rubella virus |

| id | Sequence (5' - 3') | SEQ ID NO: | species |
|-------------|----------------------------|------------|-----------------------------------|
| PMR_00007 | AGAGACCACGTCCGATCAAT | <u>692</u> | Rubella virus |
| PMR_00008 | TGAGGACGTGTAGGGCTTCT | <u>693</u> | Rubella virus |
| PMR_00009 | GTCAACGCCTACTCCTCTGG | <u>694</u> | Rubella virus |
| PMR_00010 | GTCTTGTGAGGGTGCTGGAC | <u>695</u> | Rubella virus |
| PMM_00001 | CACATTGGCATCTGAAC TCG | <u>696</u> | Measles virus |
| PMM_00002 | TCTGTTTGACCCTCCTGTCC | <u>697</u> | Measles virus |
| PMM_00003 | AGATTGCAATGCATACTACTGAGGAC | <u>698</u> | Measles virus |
| PMM_00004 | ATGCAGTGTCAATGTCTAGAGGTGT | <u>699</u> | Measles virus |
| PMM_00005 | CAATGCATACTACTGAGGACAGGA | <u>700</u> | Measles virus |
| PMM_00006 | ATGCAGTGTCAATGTCTAGAGGTG | <u>701</u> | Measles virus |
| PMM_00007 | TACCATCAGAGGTCAATTCTCAA | <u>702</u> | Measles virus |
| PMM_00008 | CTACTTCAAACACTCGGTACATGC | <u>703</u> | Measles virus |
| PMM_00009 | CATGTCGCTGTCTCTGTTAGACTT | <u>704</u> | Measles virus |
| PMM_00010 | CAAGCCTGGATTTCTTATAACACC | <u>705</u> | Measles virus |
| PMRSV_00001 | AAACCAAAGAAGAAACCAACCAT | <u>706</u> | Human respiratory syncytial virus |
| PMRSV_00002 | TGTTCTAATGTGGTTGTGTCGAG | <u>707</u> | Human respiratory syncytial virus |
| PMRSV_00003 | TGCTAAAAGAGATGGGAGAAGTG | <u>708</u> | Human respiratory syncytial virus |
| PMRSV_00004 | ATCCTTTGGTATGAGACCCTTGT | <u>709</u> | Human respiratory syncytial virus |
| PMRSV_00005 | ACAAGGGTCTCATACCAAAGGAT | <u>710</u> | Human respiratory syncytial virus |
| PMRSV_00006 | GCTAAAACTCCCCATCTTAGCAT | <u>711</u> | Human respiratory syncytial virus |
| PMRSV_00007 | TTTATGATGCAGCCAAAGCA | <u>712</u> | Human respiratory syncytial virus |
| PMRSV_00008 | TCCATGAAATTCAGGTGCAA | <u>713</u> | Human respiratory syncytial virus |

| id | Sequence (5' - 3') | SEQ ID NO: | species |
|-------------|--------------------------|------------|-----------------------------------|
| PMRSV_00009 | AAAAACACCAGCCAAAACGA | <u>714</u> | Human respiratory syncytial virus |
| PMRSV_00010 | CTGTGGGTGTTTGTGTGGAG | <u>715</u> | Human respiratory syncytial virus |
| PMRSV_00011 | CCAAAGCATATGCAGAGCAA | <u>716</u> | Human respiratory syncytial virus |
| PMRSV_00012 | TCCATGAAATTCAGGTGCAA | <u>717</u> | Human respiratory syncytial virus |
| PMPI_00001 | GCATGGAAACTAGCAGCACA | <u>718</u> | Parainfluenza |
| PMPI_00002 | GGTGTTGTGGTCTTCGAGGT | <u>719</u> | Parainfluenza |
| PMPI_00003 | GGCTCCATAGTATCATCGACAAC | <u>720</u> | Parainfluenza |
| PMPI_00004 | CCTAGAGGCCCTGTGTATACCTT | <u>721</u> | Parainfluenza |
| PMPI_00005 | ACACAACAAACAATGCAAACAAC | <u>722</u> | Parainfluenza |
| PMPI_00006 | TTAACATGCGCTTAGCAAATACA | <u>723</u> | Parainfluenza |
| PMPI_00007 | TTAGCTCACTCATTGGACACAGA | <u>724</u> | Parainfluenza |
| PMPI_00008 | GTCTCTCGTTTTGACAATGAACC | <u>725</u> | Parainfluenza |
| PMPI_00009 | TCTCACTACAAACGGTGTCAATG | <u>726</u> | Parainfluenza |
| PMPI_00010 | TCTAGATCCGCATTCTCTCTTTG | <u>727</u> | Parainfluenza |
| PMPI_00011 | ACAGATGGGTTTCATTGTCAAAC | <u>728</u> | Parainfluenza |
| PMPI_00012 | GCTTTGACCAACACTATCCAAAC | <u>729</u> | Parainfluenza |
| PMPI_00013 | GCTGAACACCCAGATTTACAAAG | <u>730</u> | Parainfluenza |
| PMPI_00014 | ACAGCTCTCCATTTTCATGGTTTA | <u>731</u> | Parainfluenza |
| PMPI_00015 | ATATGCATTTGTCAATGGAGGAG | <u>732</u> | Parainfluenza |
| PMPI_00016 | CATTTGGTGTGTAAAATGCAAGA | <u>733</u> | Parainfluenza |
| PMPI_00017 | CACAGAACACCAGAACAACAAGA | <u>734</u> | Parainfluenza |
| PMPI_00018 | TTGGGACTGTTAACCAATACACC | <u>735</u> | Parainfluenza |
| PMME_00001 | CATCCCAAAAATTGCCAGAT | <u>736</u> | Human metapneumovirus |

| id | Sequence (5' - 3') | SEQ ID NO: | species |
|------------|----------------------|------------|-----------------------|
| PMME_00002 | TTTGGGCTTTGCCTTAAATG | <u>737</u> | Human metapneumovirus |
| PMME_00003 | ACACCCTCATCATTGCAACA | <u>738</u> | Human metapneumovirus |
| PMME_00004 | GCCCTTCTGACTGTGGTCTC | <u>739</u> | Human metapneumovirus |
| PMME_00005 | CGACACAGCAGCAGGAATTA | <u>740</u> | Human metapneumovirus |
| PMME_00006 | TCAAAGCTGCTTGACACTGG | <u>741</u> | Human metapneumovirus |

Please replace Table 20, beginning on page 61 and bridging to page 66, with a new Table 20 as follows:

Table 20. Exemplary primers for non-SARS-CoV infectious organism damaging the subject's immune system

| id | sequence (5' - 3') | SEQ ID NO: | species |
|-------------|----------------------------|------------|---------|
| PMTTV_00001 | TGGGGCCAGACTTCGCCATA | <u>742</u> | TTV |
| PMTTV_00002 | AGCTTCCGCCGAGGATGACC | <u>743</u> | TTV |
| PMTTV_00003 | CTTGGGGGCTCAACGCCTTC | <u>744</u> | TTV |
| PMTTV_00004 | GCGAAGTCTGGCCCCACTCA | <u>745</u> | TTV |
| PMTTV_00005 | CCACAGGCCAACCGAATGCT | <u>746</u> | TTV |
| PMTTV_00006 | AGCCCGAATTGCCCTTGAC | <u>747</u> | TTV |
| PMTTV_00007 | AGCGAATCCTGGGAGTCAAACCTCAG | <u>748</u> | TTV |
| PMTTV_00008 | GGCCTCGTACTCTCTTTCCAGTCA | <u>749</u> | TTV |
| PMTTV_00009 | GCCCCTTTGCATACCACTCAGACAT | <u>750</u> | TTV |
| PMTTV_00010 | TGGAATGTGAGTTCCGGTGAGTTGT | <u>751</u> | TTV |
| PMTTV_00011 | TGTCAGTAACAGGGGTCGCCATAGA | <u>752</u> | TTV |
| PMTTV_00012 | TGTGACGTATGGACGACCTTTGACC | <u>753</u> | TTV |
| PMV_11047 | CACAGACAGAGGAGAAGGCAAC | <u>754</u> | TTV |
| PMV_11048 | AATAGGCACATTACTACTACCTCCTG | <u>755</u> | TTV |

| id | sequence (5' - 3') | SEQ ID NO: | species |
|--------------|-----------------------------|------------|---------|
| PMTP_00001 | GCGGTCGGTAGGAGGATAAAGGAAA | 756 | TP |
| PMTP_00002 | CCGGGGATTGTGTCTACAGGGTTTCT | 757 | TP |
| PMTP_00003 | CAGACGCTCATCCAACCTCTGAGAA | 758 | TP |
| PMTP_00004 | CCGTTGTACCGTCTTTTGGACGTT | 759 | TP |
| PMTP_00005 | CACGCTCTACCTCATTCGAGAGCAA | 760 | TP |
| PMTP_00006 | GTTGTGTTGCAACGAACACGCTACA | 761 | TP |
| PMTP_00007 | AGCGGTCGGTAGGAGGATAAAGGAA | 762 | TP |
| PMTP_00008 | ACCGGGGATTGTGTCTACAGGGTTTC | 763 | TP |
| PMV_11025 | AACACGATCCGCTACGACTACTAC | 764 | TP |
| PMV_11026 | CCCTATACCCGTTTCGCAATCAAAG | 765 | TP |
| PMHIV1_00001 | ATGGGCGCAGCCTCAATGAC | 766 | HIV1 |
| PMHIV1_00002 | CCCCAAATCCCCAGGAGCTG | 767 | HIV1 |
| PMHIV1_00003 | GGGACAGCTACAACCATCCCTTCAG | 768 | HIV1 |
| PMHIV1_00004 | GACCTGATTGCTGTGTCTGTGTCA | 769 | HIV1 |
| PMHIV1_00005 | GGGATGGAAAGGATCACCAGCAATA | 770 | HIV1 |
| PMHIV1_00006 | GTCTGGTGTGGTAAGTCCCCACCTC | 771 | HIV1 |
| PMHIV1_00007 | AAGGATCAACAGCTCCTGGGGATTT | 772 | HIV1 |
| PMHIV1_00008 | TTCTTGCTGGTTTTGCGATTCTTCA | 773 | HIV1 |
| PMV_11055 | TAATCCACCTATCCCAGTAGGAGAAAT | 774 | HIV1 |
| PMV_11056 | GGTCCTTGCTTTATGTCCAGAATGC | 775 | HIV1 |
| PMV_11057 | TGGGAAGTTCAATTAGGAATACCAC | 776 | HIV1 |
| PMV_11058 | TCCTACATACAAATCATCCATGTATTG | 777 | HIV1 |
| PMHGV_00001 | GCCGGCGATGACTGCTTGAT | 778 | HGV |
| PMHGV_00002 | TCCGGAAGTCCGTGGTCAGG | 779 | HGV |
| PMHGV_00003 | ACGGTGGGAGTCGCGTTGAC | 780 | HGV |
| PMHGV_00004 | GGCCACGCAAACCAACAAGG | 781 | HGV |

| id | sequence(5' - 3') | SEQ ID NO: | species |
|-------------|----------------------------|------------|---------|
| PMHGV_00005 | CGGCCAAAAGGTGGTGGATG | <u>782</u> | HGV |
| PMHGV_00006 | CGGGCTCGGTTTAACGACGA | <u>783</u> | HGV |
| PMHGV_00007 | GCCACGGGCAAAATCAGTGG | <u>784</u> | HGV |
| PMHGV_00008 | TGTCGCGATCCGATGATCCA | <u>785</u> | HGV |
| PMHGV_00009 | CGCGTGTGAGCTAAAGTGGGAAAAGT | <u>786</u> | HGV |
| PMHGV_00010 | ATCGTCACCAACAGGAAGACCATGA | <u>787</u> | HGV |
| PMHGV_00011 | TCGCTCTCGGGTTGGTTTTGTATTC | <u>788</u> | HGV |
| PMHGV_00012 | CATCCACCTTAGGCTCCCTGTTGAC | <u>789</u> | HGV |
| PMV_11045 | GGGTTGGTAGGTCTGTAATCCC | <u>790</u> | HGV |
| PMV_11046 | GTACGTGGGCGTCGTTTGC | <u>791</u> | HGV |
| PMV_11001 | CCTTTCCACCATCCAGCAGT | <u>792</u> | HEV |
| PMV_11002 | CGAGCTTTACCCACCTTCAGC | <u>793</u> | HEV |
| PMHEV_00001 | CTGGCGGTGGGCTCTGTCTAT | <u>794</u> | HEV |
| PMHEV_00002 | ACCGAGGCGGGAGCAAGTCT | <u>795</u> | HEV |
| PMHEV_00003 | ACGGGCGGATCGATTGTGAG | <u>796</u> | HEV |
| PMHEV_00004 | GGCAGCGACATAGCGCACCT | <u>797</u> | HEV |
| PMHEV_00005 | AGCTCACCACCACGGCTGCT | <u>798</u> | HEV |
| PMHEV_00006 | CTGAGACGACGGGGCGAGAG | <u>799</u> | HEV |
| PMHEV_00007 | ATCGCGCCCCTTTTCTGTCC | <u>800</u> | HEV |
| PMHEV_00008 | GGGGGCGACCATCAAGTGTG | <u>801</u> | HEV |
| PMHDV_00001 | GACGGGCCGGCTGTTCTTCT | <u>802</u> | HDV |
| PMHDV_00002 | GACTCCGGGCCTGGGAAGAG | <u>803</u> | HDV |
| PMHDV_00003 | ACTCCGGCCGAAAGGTCTGAG | <u>804</u> | HDV |
| PMHDV_00004 | GGCGGAACACCCACCGACTA | <u>805</u> | HDV |
| PMHDV_00005 | CCATGACTCTGGAGACATCCTGGAA | <u>806</u> | HDV |
| PMHDV_00006 | CGTCAGAGCTCTCTGTTGCTGAAG | <u>807</u> | HDV |

| id | sequence (5' - 3') | SEQ ID NO: | species |
|--------------|---------------------------|------------|---------|
| PMHDV_00007 | CCTTCTCTCGTCTTCCTCGGTCAAC | 808 | HDV |
| PMHDV_00008 | CCGAACGGACCAGATGGAGATAGAC | 809 | HDV |
| PMHDV_00009 | GCTCCCGAGAGGGATAAAACGGTAA | 810 | HDV |
| PMHDV_00010 | GAGTGCTCTCCAACTTGGCAGTTG | 811 | HDV |
| PMHDV_00011 | TCTCGTCTTCCTCGGTCAACCTCTT | 812 | HDV |
| PMHDV_00012 | CCGAACGGACCAGATGGAGATAGAC | 813 | HDV |
| PMV_11041 | AACATTCCGAAGGGGACCGT | 814 | HDV |
| PMV_11042 | GGCATCCGAAGGAGGACG | 815 | HDV |
| PMHCV_00001 | GGCGCTGGAAGAGGGTCTACTACC | 816 | HCV |
| PMHCV_00002 | TGTTCAAGCTGATCCCTGGCTATGA | 817 | HCV |
| PMHCV_00003 | ACATCTGGGACTGGATATGCGAGGT | 818 | HCV |
| PMHCV_00004 | ATCCTCATCGTCCCGTTTTTGACAT | 819 | HCV |
| PMHCV_00005 | TGTGCCAGGACCATCTTGAATTTTG | 820 | HCV |
| PMHCV_00006 | AGGCGGATCAAACACTTCCACATCT | 821 | HCV |
| PMHCV_00007 | GGGGTGCAAATGATACGGATGTCTT | 822 | HCV |
| PMHCV_00008 | AGAGTATGTGGCTTCCGGATGCTTG | 823 | HCV |
| PMHCV_00009 | ACACGCCGTGGGCCTATTCA | 824 | HCV |
| PMHCV_00010 | GCCGGGACCTTGGTGCTCTT | 825 | HCV |
| PMHCV_00011 | CACGCCGTGGGCCTATTCA | 826 | HCV |
| PMHCV_00012 | GCCGGGACCTTGGTGCTCTT | 827 | HCV |
| PMV_11039 | CTCGCAAGCACCTATCAGGCAGT | 828 | HCV |
| PMV_11040 | GCAGAAAGCGTCTAGCCATGGCGT | 829 | HCV |
| PMHCMV_00001 | GCGCCTGCTGCTCGAAATGT | 830 | HCMV |
| PMHCMV_00002 | GTCGCGGCTGTTGCGGTAGT | 831 | HCMV |
| PMHCMV_00003 | CCCCACGTCCATCTGCGTCT | 832 | HCMV |
| PMHCMV_00004 | GCCCCAGCAGTCTCACCAG | 833 | HCMV |

| id | sequence (5' - 3') | SEQ ID NO: | species |
|--------------|----------------------------|------------|---------|
| PMHCMV_00005 | GCTCACGCACCCTGGAGGAC | 834 | HCMV |
| PMHCMV_00006 | AGTTCCAGCCCACGCACCAG | 835 | HCMV |
| PMHCMV_00007 | GTGCAGTTTtaggtggcagttcatgc | 836 | HCMV |
| PMHCMV_00008 | GGAAAGGGGAGGGTAGAAACGTGAG | 837 | HCMV |
| PMHCMV_00009 | TGTGATTGCGTGTGCAGTTTtaggtg | 838 | HCMV |
| PMHCMV_00010 | GGGGAGGGTAGAAACGTGAGTCTCC | 839 | HCMV |
| PMV_11051 | ATTCCAAGCGGCCTCTGATAA | 840 | HCMV |
| PMV_11052 | TCTTCCTCTGGGGCAACTTCC | 841 | HCMV |
| PMHBV_00001 | TCGCAGTCCCCAACCTCCAA | 842 | HBV |
| PMHBV_00002 | CAGGGTCCCGTGCTGGTTGT | 843 | HBV |
| PMHBV_00003 | GCAGCCGGTCTGGAGCAAAA | 844 | HBV |
| PMHBV_00004 | GCAGACGGAGAAGGGGACGA | 845 | HBV |
| PMHBV_00005 | CGCCTCATTTTgCGGGTCAC | 846 | HBV |
| PMHBV_00006 | TGGTTGGCTTGTGGCCAGTG | 847 | HBV |
| PMHBV_00007 | ATCAAGGTATGTTGCCCCGTTGTCC | 848 | HBV |
| PMHBV_00008 | AGGCCCACTCCCATAGGTATTTTGC | 849 | HBV |
| PMHBV_00009 | CCTAGGACCCCTGCTCGTGTTACAG | 850 | HBV |
| PMHBV_00010 | GCGATAACCAGGACAAATTGGAGGA | 851 | HBV |
| PMHBV_00011 | CTGCGCACCATTATCATGCAACTTT | 852 | HBV |
| PMHBV_00012 | AGTAGATCCCGGACGGAAGGAAAGA | 853 | HBV |
| PMV_11037 | GTTCAAGCCTCCAAGCTGTG | 854 | HBV |
| PMV_11038 | TCAGAAGGCAAAAAAGAGAGTAACT | 855 | HBV |
| PMHAV_00001 | GATGTTTGGGACGTCACCTT | 856 | HAV |
| PMHAV_00002 | CTGGATGAGAGCCAGTCCTC | 857 | HAV |
| PMHAV_00003 | ATTGCATTGGCAACCAAAAT | 858 | HAV |
| PMHAV_00004 | ATCTCATTGGGCATCCTGAC | 859 | HAV |

| id | sequence (5' - 3') | SEQ ID NO: | species |
|-------------|----------------------------|------------|---------|
| PMHAV_00005 | GACTGGAGGTTGGGAAACAA | <u>860</u> | HAV |
| PMHAV_00006 | AGCAGCCAGAGAGAATCCAA | <u>861</u> | HAV |
| PMHAV_00007 | TAAGCATTTTTCCCGCAAAG | <u>862</u> | HAV |
| PMHAV_00008 | AGGCATTCATGACCCATCTC | <u>863</u> | HAV |
| PMHAV_00009 | CCAACCAAATATCATTTCAGGTAGAC | <u>864</u> | HAV |
| PMHAV_00010 | GACTTCGTGTACCTATTCACCTCGAT | <u>865</u> | HAV |
| PMHAV_00011 | GGGTTTCCTTATGTTCAAGAAAAAT | <u>866</u> | HAV |
| PMHAV_00012 | CCAAACTTTCTCTAATGGTCTCAA | <u>867</u> | HAV |
| PMV_11035 | TTTTGCTCCTCTTTACCATGCTATG | <u>868</u> | HAV |
| PMV_11036 | GGAAATGTCTCAGGTACTTTCTTTG | <u>869</u> | HAV |
| PMEBV_00001 | AACCCAATAGCATGACAGCCAATCC | <u>870</u> | EBV |
| PMEBV_00002 | TCAGCCCCAGAGACACGGTATATGA | <u>871</u> | EBV |
| PMEBV_00003 | TGAACCTGGGACCTATTGATGCAGA | <u>872</u> | EBV |
| PMEBV_00004 | CAGGGGAATCTCTGCCAACTTTGAG | <u>873</u> | EBV |
| PMEBV_00005 | TGCACAGTGACAGTGGGAGAAACAC | <u>874</u> | EBV |
| PMEBV_00006 | AAGAATGGAAAGGGTTGGCAGTGTG | <u>875</u> | EBV |
| PMEBV_00007 | GTGCACAGTGACAGTGGGAGAAACA | <u>876</u> | EBV |
| PMEBV_00008 | AAGAATGGAAAGGGTTGGCAGTGTG | <u>877</u> | EBV |
| PMV_11053 | CCCACGCGCGCATAATG | <u>878</u> | EBV |
| PMV_11054 | TTCACTTCGGTCTCCCTTAG | <u>879</u> | EBV |
| PMB19_00001 | TGGGCCGCCAAGTACAGGAA | <u>880</u> | B19 |
| PMB19_00002 | GGGTTGCCCGCCTAAATGG | <u>881</u> | B19 |
| PMB19_00003 | CCCTATTAGTGGGGCAGCATGTGTT | <u>882</u> | B19 |
| PMB19_00004 | CCACCAAGCTTTTCCCTGCTACATC | <u>883</u> | B19 |
| PMB19_00005 | CAGTGTCACAGCCATACCACCACTG | <u>884</u> | B19 |
| PMB19_00006 | TGCTGGGTTCTTTATTGGGGAAAT | <u>885</u> | B19 |

| id | sequence (5' - 3') | SEQ ID NO: | species |
|-------------|---------------------------|------------|---------|
| PMB19_00007 | CCCATTGCATTAATGTAGGGGCTTG | <u>886</u> | B19 |
| PMB19_00008 | ATCACTTTCCACCATTGCGCACTT | <u>887</u> | B19 |
| PMV_11049 | CCTTTCCACCATCCAGCAGT | <u>888</u> | B19 |
| PMV_11050 | CGAGCTTTACCCACCTTCAGC | <u>889</u> | B19 |

Please replace Table 21, beginning on page 66 and bridging to page 68, with a new Table 21 as follows:

Table 21. Exemplary primers for non-SARS-CoV coronaviridae virus

| seqid | sequence (5' - 3') | SEQ ID NO: |
|-------------|----------------------------|------------|
| PMIBV_00001 | GGAACAGGACCTGCCGCTGA | <u>890</u> |
| PMIBV_00002 | ATCAGGTCCGCCATCCGAGA | <u>891</u> |
| PMIBV_00003 | AAAGGTGGAAGAAAACCAGTCCCAGA | <u>892</u> |
| PMIBV_00004 | GCCATCCGAGAATCGTAGTGGGTATT | <u>893</u> |
| PMMHV_00001 | CAGCGCCAGCCTGCCTCTAC | <u>894</u> |
| PMMHV_00002 | TGCTGCACTGGGCACTGCTT | <u>895</u> |
| PMMHV_00003 | GGAAATTACCGACTGCCCTCAAACA | <u>896</u> |
| PMMHV_00004 | TGATTATTTGGTCCACGCTCGGTTT | <u>897</u> |
| PMEQ_00001 | TCCCGCGCATCCAGTAGAGC | <u>898</u> |
| PMEQ_00002 | CTGCGGCTTTGTGGCATCCT | <u>899</u> |
| PMEQ_00003 | TTTGCTGAAGGACAAGGTGTGCCTA | <u>900</u> |
| PMEQ_00004 | CCAGAAGACTCCGTCAATGTTGGTG | <u>901</u> |
| PMCA_00001 | AAAAACGTGGTCGTTCCAATTCTCG | <u>902</u> |
| PMCA_00002 | CCATGCGATAGCGGCTTTGTCTATT | <u>903</u> |
| PMCA_00003 | TGGGAACGGTGCCAAGCATT | <u>904</u> |
| PMCA_00004 | GCCACCTCTGATGGACGAGCA | <u>905</u> |
| PMFE_00001 | CGCGTCAACTGGGGAGATGAA | <u>906</u> |
| PMFE_00002 | GCGCGCCTGTCTGTTCCAAT | <u>907</u> |
| PMFE_00003 | GAGTCTTCTGGGTGCAAAGGATGG | <u>908</u> |

| seqid | sequence (5'-3') | SEQ ID NO: |
|--------------|---------------------------|------------|
| PMFE 00004 | CCCCTGGATTGAGACCTGTTTCTTG | <u>909</u> |
| PMPEDV 00001 | GCAGCATTGCTCTTTGGTGGTAATG | <u>910</u> |
| PMPEDV 00002 | TGCTGAATGGTTTCACGCTTGTTCT | <u>911</u> |
| PMPEDV 00003 | CCGCAAACGGGTGCCATTAT | <u>912</u> |
| PMPEDV 00004 | TCGCCGTGAGGTCCTGTTCC | <u>913</u> |
| PMPTGV 00001 | TCGCTCCAATTCCC GTGGTC | <u>914</u> |
| PMPTGV 00002 | ACGTTGGCCCTTCACCATGC | <u>915</u> |
| PMPTGV 00003 | CAAGCATTACCCACAATTGGCTGAA | <u>916</u> |
| PMPTGV 00004 | TTCTTTTGCCACTTCTGATGGACGA | <u>917</u> |
| PMBOV 00001 | TTCTTTTAAAACAGCCGATGGCAAC | <u>918</u> |
| PMBOV 00002 | TCGGAATAGCCTCATCGCTACTTGG | <u>919</u> |
| PMBOV 00003 | TTCCGCCTGGCACGGTACTC | <u>920</u> |
| PMBOV 00004 | TGGCTTAGCGGCATCCTTGC | <u>921</u> |
| PMFIPV 00001 | CACCATGGCCTCAGCCTTGA | <u>922</u> |
| PMFIPV 00002 | GTGCCGCCAACCTGCCAGTA | <u>923</u> |
| PMFIPV 00003 | GGTCTTGGCACTGTGGATGATGATT | <u>924</u> |
| PMFIPV 00004 | GAAAAAGGGACAGCTACAGCGGATG | <u>925</u> |
| PMR 00001 | CCCAATCAGAATTTTGAGGCTCTG | <u>926</u> |
| PMR 00002 | AGCGAATTGCACCTGAATACTGCAA | <u>927</u> |
| PMR 00003 | TGACCAAACCGAGCGTGCAG | <u>928</u> |
| PMR 00004 | CAGTGGCGGGGATTCCATTG | <u>929</u> |
| PMPHEV 00001 | AGCGTCAACTGCTGCCACGA | <u>930</u> |
| PMPHEV 00002 | AGTACCGTGCCAGGCGGAAA | <u>931</u> |
| PMPHEV 00003 | AAGGTGTGCCTATTGCACCAGGAGT | <u>932</u> |
| PMPHEV 00004 | ACTAGCGACCCAGAAGACTCCGTCA | <u>933</u> |
| PMPV 00001 | AGAAGACCACTTGGGCTGACCAAAC | <u>934</u> |
| PMPV 00002 | TTGGCAATAGGCACTCCTTGTCCTT | <u>935</u> |
| PMPV 00003 | GCGCCAGCCTGCCTCTATTG | <u>936</u> |
| PMPV 00004 | TGGGGCCCCCTCTTTCCAAAA | <u>937</u> |

| seqid | sequence (5'-3') | <u>SEQ ID NO:</u> |
|--------------|---------------------------|-------------------|
| PMTK 00001 | ATGGCTCACCGCCGGTATTG | <u>938</u> |
| PMTK 00002 | TGGGCGTCACTCTGCTTCCA | <u>939</u> |
| PMTK 00003 | GCTAAGGCTGATGAAATGGCTCACC | <u>940</u> |
| PMTK 00004 | TCCAAAAAGACAAGCATGGCTGCTA | <u>941</u> |
| PMSDAV 00001 | TCTATGTTGAAGGCTCGGGAAGGTC | <u>942</u> |
| PMSDAV 00002 | TACTTGCTTAGGCTGTCCGGCATCT | <u>943</u> |
| PMSDAV 00003 | AGCAGTGCCCAGTGCAGCAG | <u>944</u> |
| PMSDAV 00004 | TGGGTTTCATCAACGCCACCA | <u>945</u> |